

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 21:14:47 ; Search time 704.5 Seconds
(without alignments)
8509.834 Million cell updates/sec

Title: 09-833799-13C
Perfect score: 206
Sequence: 1 gctcgagccatgttatggac.....gcaaggtgttattatcctag 206

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vi:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pln:*
35: em.htg.rod:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	37.6	18.3	90551	8	ATT5K18	AL022580 Arabidops
2	37.6	18.3	96574	8	ATT18B16	AL021687 Arabidops
3	37.6	18.3	199382	8	ATCHRIV50	AL161550 Arabidops
4	35.8	17.4	321003	2	PFMAL4P3	AL035476 Plasmodiu
5	35.2	17.1	216340	2	AC073754	AC073754 Mus muscu
C 6	35.2	17.1	238142	2	AL611930	AL611930 Mus muscu
C 7	34.8	16.9	32609	9	AP000257	AP000257 Homo sapi
C 8	34.8	16.9	100000	9	AP000098	AP000098 Homo sapi
C 9	34.8	16.9	100000	9	AP000174	AP000174 Homo sapi
C 10	34.8	16.9	340000	9	AP001712	AP001712 Homo sapi
11	34.6	16.8	181773	10	AC087336	AC087336 Mus muscu
12	34	16.5	158420	2	AC128340	AC128340 Rattus no
13	33.8	16.4	153551	9	AC092675	AC092675 Homo sapi
C 14	33.8	16.4	163140	9	AL354926	AL354926 Human DNA
15	33.6	16.3	169242	2	AC117956	AC117956 Rattus no
C 16	33.4	16.2	34122	3	AF100673	AF100673 Caenorhab
17	33	16.0	9056	3	U50192	U50192 Caenorhabdi
C 18	33	16.0	68850	2	AC015606	AC015606 Homo sapi
C 19	33	16.0	95983	2	AC127176	AC127176 Rattus no
20	33	16.0	174900	2	AC110319	AC110319 Rattus no
C 21	33	16.0	212404	10	AC090127	AC090127 Mus muscu
22	33	16.0	213265	2	AC100386	AC100386 Mus muscu
C 23	32.8	15.9	10875	1	AE005515	AE005515 Escherich
C 24	32.8	15.9	16950	6	AR204270	AR204270 Sequence
25	32.6	15.8	75344	2	AC108788	AC108788 Mus muscu
26	32.6	15.8	90422	9	AC023880	AC023880 Homo sapi
C 27	32.6	15.8	131133	2	AC079746	AC079746 Homo sapi
C 28	32.6	15.8	159480	9	AC021843	AC021843 Homo sapi
C 29	32.6	15.8	168406	2	AC090770	AC090770 Homo sapi
C 30	32.6	15.8	170337	2	AP001378	AP001378 Homo sapi
31	32.6	15.8	170843	9	AC027216	AC027216 Homo sapi
C 32	32.6	15.8	176562	9	AC084864	AC084864 Homo sapi
C 33	32.6	15.8	176715	2	AC073474	AC073474 Homo sapi
34	32.6	15.8	177013	2	AC096176	AC096176 Rattus no
C 35	32.6	15.8	214162	9	AC084865	AC084865 Homo sapi
36	32.4	15.7	89672	9	AC005872	AC005872 Homo sapi
C 37	32.4	15.7	112746	2	AC130995	AC130995 Rattus no
38	32.4	15.7	127049	2	AC129828	AC129828 Rattus no
C 39	32.4	15.7	216031	9	AC011328	AC011328 Homo sapi
C 40	32.2	15.6	12318	3	CET23H4	Z83240 Caenorhabdi
41	32.2	15.6	154139	2	AC095797	AC095797 Rattus no
42	32	15.5	151675	9	AP000470	AP000470 Homo sapi
43	32	15.5	154096	2	AC119523	AC119523 Rattus no
C 44	32	15.5	165929	2	AC118484	AC118484 Rattus no
45	32	15.5	340000	9	AP001689	AP001689 Homo sapi
46	31.8	15.4	176350	2	AC092513	AC092513 Papio cyn
47	31.8	15.4	185829	2	AC094911	AC094911 Rattus no
48	31.8	15.4	188412	2	AC120688	AC120688 Rattus no
C 49	31.8	15.4	193958	2	AC084753	AC084753 Mus muscu
50	31.6	15.3	157750	9	AL512599	AL512599 Human DNA
51	31.6	15.3	205615	2	AC108799	AC108799 Mus muscu
52	31.4	15.2	3277	8	SCYNL298W	Z71574 S.cerevisia
53	31.4	15.2	3858	8	SCCLA4	X82499 S.cerevisia
54	31.4	15.2	30003	8	SCU23084	U23084 Saccharomyc
55	31.4	15.2	64656	2	AC102032	AC102032 Mus muscu
56	31.4	15.2	72312	9	AL138731	AL138731 Human DNA
57	31.4	15.2	173368	9	AC091647	AC091647 Homo sapi
58	31.4	15.2	185479	2	AP001484	AP001484 Homo sapi
59	31.4	15.2	190519	2	AC099591	AC099591 Mus muscu
C 60	31.4	15.2	200512	2	AL844585	AL844585 Mus muscu
61	31.2	15.1	591	8	AF208338	AF208338 Streptoca
C 62	31.2	15.1	876	6	AX097725	AX097725 Sequence
C 63	31.2	15.1	876	9	AF227139	AF227139 Homo sapi
64	31.2	15.1	2954	9	HSM80441	AL833130 Homo sapi
65	31.2	15.1	31041	9	AC104114	AC104114 Homo sapi

C 66	31.2	15.1	80436	9	AC114759	AC114759 Homo sapi
C 67	31.2	15.1	83905	2	AC025337	AC025337 Homo sapi
C 68	31.2	15.1	94341	9	AL158036	AL158036 Human DNA
C 69	31.2	15.1	109042	2	AC094194	AC094194 Rattus no
C 70	31.2	15.1	110000	2	AC113004_0	AC113004 Mus muscu
C 71	31.2	15.1	142992	9	AC004838	AC004838 Homo sapi
C 72	31.2	15.1	144544	8	AC119071	AC119071 Oryza sat
C 73	31.2	15.1	146118	2	AC011729	AC011729 Homo sapi
C 74	31.2	15.1	146525	2	AC022189	AC022189 Homo sapi
C 75	31.2	15.1	153232	9	AC024086	AC024086 Homo sapi
C 76	31.2	15.1	154772	2	AC106955	AC106955 Rattus no
C 77	31.2	15.1	176813	2	AC102554	AC102554 Mus muscu
C 78	31.2	15.1	181936	2	AL360090	AL360090 Homo sapi
C 79	31.2	15.1	184655	2	AC079379	AC079379 Homo sapi
C 80	31.2	15.1	185124	9	AC009358	AC009358 Human Chr
C 81	31.2	15.1	211654	2	AL591103	AL591103 Homo sapi
C 82	31.2	15.1	222585	2	AC101391	AC101391 Mus muscu
C 83	31	15.0	83684	9	AC105290	AC105290 Homo sapi
C 84	31	15.0	108302	2	AP004188	AP004188 Oryza sat
C 85	31	15.0	133401	9	AC079257	AC079257 Homo sapi
C 86	31	15.0	193577	8	AP004365	AP004365 Oryza sat
C 87	31	15.0	196614	2	AL844889	AL844889 Mus muscu
C 88	31	15.0	204483	10	AL671990	AL671990 Mouse DNA
C 89	31	15.0	206682	2	AC060790	AC060790 Homo sapi
C 90	30.8	15.0	3071	14	AY053369	AY053369 Acute bee
C 91	30.8	15.0	3071	14	AY053370	AY053370 Acute bee
C 92	30.8	15.0	14408	3	CELTMY1A	D38539 Caenorhabdi
C 93	30.8	15.0	96987	9	AC096573	AC096573 Homo sapi
C 94	30.8	15.0	102117	2	CEY105E8_6	Continuation (7 of
C 95	30.8	15.0	115666	2	AC105744	AC105744 Oryza sat
C 96	30.8	15.0	139948	2	AC121427	AC121427 Rattus no
C 97	30.8	15.0	144781	9	HSJ585114	AL121782 Human DNA
C 98	30.8	15.0	179089	2	AC084227	AC084227 Homo sapi
C 99	30.8	15.0	191335	2	AC010700	AC010700 Drosophil
C 100	30.8	15.0	206647	2	AC124907	AC124907 Equus cab

ALIGNMENTS

RESULT 1	ATT5K18	90551 bp	DNA	linear	PLN 10-MAR-2000
LOCUS	Arabidopsis thaliana	DNA chromosome 4,	BAC clone	T5K18	(ESSA
DEFINITION	project).				
ACCESSION	AL022580				
VERSION	AL022580.1	GI:3080352			
KEYWORDS	Arabidopsis thaliana.				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1 (bases 1 to 90551)				
AUTHORS	Bevan,M., Van Der Schueren,J., Chuang,Y.J., Aert,R., Defoor,E., Robben,J., Volckaert,G., Bancroft,I., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 90551)				
AUTHORS	EU Arabidopsis sequencing,project.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de project				
COMMENT	Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk				
FEATURES	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/. Location/Qualifiers				
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	/gene="AT4g19250"	
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Best Local Similarity 53.4%; Pred. No. 0.48;
Matches 79; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 5 GAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCAGGACACAGATGATTCGGT 64
Db 112137 GACTCATTATATGATCACATATAAGAACAAAGGTGTGAGCCGATCATACATAGCCTATGGT 112196
QY 65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACATAATTGGGTGGATTGGCAACAAAC 124
Db 112197 TCGAGATCAAACTAATCCACTAAGCTTCAAGACTAACTTACATCTGTTGGCAACCAAT 112256
QY 125 TTCCTGTGACTAACAGGTCCATAGTTT 152
Db 112257 CTACTCTATGTACAGGTTTCTAGTATT 112284

RESULT 4
PFMAL4P3
LOCUS
DEFINITION
Plasmodium falciparum 3D7 chromosome 4, *** SEQUENCING IN PROGRESS
***, in unordered pieces.
AL035476
AL035476.6 GI:5763808
HTG; HTGS PHASE1.
Plasmodium falciparum 3D7.
Plasmodium falciparum 3D7.
ORGANISM
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 321003)
AUTHORS
Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M.
and Barrell, B.
Direct Submission
Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK
COMMENT
On Aug 24, 1999 this sequence version replaced gi:5731899.
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This
sequence is unfinished and does not necessarily represent the
correct sequence. Work on the sequence is in progress and the
release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc.
Order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence

JOURNAL
MEDLINE
REFERENCE
AUTHORS

Nature 405 (6784), 311-319 (2000)
20289799
2 (bases 1 to 340000)
Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
Zimmermann,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,
Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
Yaspo,M.L.

TITLE

JOURNAL

Direct Submission
Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
Genetics (addresses see below)
On May 30, 2000 this sequence version replaced gi:7717325.
The chromosome 21 mapping and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagami-hara 228-8555, Japan,
* e.mail: hattori@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
and
* Institute of Molecular Biotechnology, Genome Analysis, *
Beutenbergstrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
and

COMMENT

* Keio University School of Medicine, Molecular Biology, * Tokyo
160-8582, Japan,
* e.mail: nshimizue@dm-b-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
and
* GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@gbf.de
* URL: http://genome.gbf.de/
and
* Max-Planck Institute for Molecular Genetics,
* Ihnestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chr21@molgen.mpg.de
* URL: http://chr21.rz-berlin.mpg.de/
AL163257: Submitted (10-APR-2000).
Location/Qualifiers

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Db 221465 CAAGAA 221460

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ACCESSION
VERSION
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KEYWORDS
SOURCE
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ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 181773)
REFERENCE
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
Mus musculus chromosome 6, clone RP23-44607
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REFERENCE
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
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Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
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Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
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|||||
Db 221585 CAAGAAAACAACCTTCTGTCAAAGATCAGTAAACCGAGACTCATCAACAGATCCAAAGT 221526

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|||||
Db 221525 TGCAAGCCTTTTCAAAATTTTACAAAGGAATCAGTTTCCAAAGATTTCCCCCATATTTC 221466

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RESULT 11
AC087336
LOCUS
DEFINITION
AC087336 Mus musculus chromosome 6, clone RP23-44607, linear ROD 14-MAR-2002
ACCESSION
VERSION
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KEYWORDS
SOURCE
HTG.
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 181773)
REFERENCE
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
Mus musculus chromosome 6, clone RP23-44607
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REFERENCE
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
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TITLE

JOURNAL

REFERENCE

AUTHORS

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Submitted (28-DEC-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 181773)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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TITLE

JOURNAL

COMMENT

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Submitted (14-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 14, 2002 this sequence version replaced gi:18584052.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11595
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Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 158420)
Worley, K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GZDR
Center clone name: CH230-188010
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 84495 bases at least Q40
Consensus quality: 88503 bases at least Q30
Consensus quality: 91376 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 72 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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misc_feature 7016. .7361 /note="match to EST BG911822 (NID:gl4292298)"
repeat_region 7357. .7613 /note="match to EST BE882861 (NID:gl0331741)"
repeat_region 7798. .8160 /rpt_family="L1"
repeat_region 8951. .9000 /rpt_family="L1"
misc_feature 9006. .9207 /note="match to EST BG717868 (NID:gl3997055)"
misc_feature 9006. .9180 /note="similar to Sus scrofa EST BF191863 (NID:gl1075232)"
repeat_region 9450. .9649 /rpt_family="MIR"
repeat_region 9716. .10135 /rpt_family="L1"
repeat_region 10180. .10268 /rpt_family="MaLR"
repeat_region 10301. .11060 /rpt_family="ERV1"
repeat_region 11051. .11103 /rpt_family="TATATG)n"
repeat_region 11117. .11406 /rpt_family="MaLR"
repeat_region 11595. .11637 /rpt_family="T-rich"
repeat_region 11948. .12042 /rpt_family="L2"
repeat_region 13297. .13545 /rpt_family="L2"
repeat_region 13575. .13727 /rpt_family="L2"
repeat_region 13840. .13898 /rpt_family="MIR"
repeat_region 14059. .14267 /rpt_family="L2"
repeat_region 16466. .17218 /rpt_family="ERV1"
repeat_region 17842. .18048 /rpt_family="ERV1"
repeat_region 20757. .20779 /rpt_family="T)n"
repeat_region 22097. .22241 /rpt_family="MIR"
repeat_region 23353. .23861 /rpt_family="L1"
repeat_region 23860. .25086 /rpt_family="L1"
repeat_region 25113. .25687 /rpt_family="L1"
repeat_region 25725. .25802 /rpt_family="MER1_type"
repeat_region 26137. .26910 /rpt_family="L1"
repeat_region 27520. .27568 /rpt_family="TA)n"
repeat_region 27646. .27844

repeat_region /rpt_family="L1"
misc_feature 28373. .28755 /rpt_family="MaLR"
repeat_region 28835. .28946 /note="match to EST BG717868 (NID:gl3997055)"
repeat_region 29178. .29599 /rpt_family="L2"
repeat_region 29774. .29991 /rpt_family="L2"
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repeat_region 30286. .30570 /rpt_family="Alu"
repeat_region 30406. .30429 /rpt_family="(A)n"
repeat_region 30634. .30670 /rpt_family="AT_rich"
repeat_region 31007. .31314 /rpt_family="Alu"
repeat_region 31819. .32507 /rpt_family="L1"
repeat_region 32509. .32528 /rpt_family="(CA)n"
repeat_region 32529. .32557 /rpt_family="(A)n"
repeat_region 33125. .33259 /rpt_family="MIR"
repeat_region 34391. .34455 /rpt_family="MER1_type"
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repeat_region 35270. .35346 /rpt_family="Mariner"

Query Match 16.4%; Score 33.8; DB 9; Length 153551;
Best Local Similarity 52.5%; Pred. No. 7.8;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 27 GAGTTCTTGGTCAATTCAGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACT 86
Db 98660 GAGTTGTGCCAGGATAGAGAAAGCAGCTGAGGGGCTGAAGGAAGGGGCACAGGCTGG 98719
QY 87 AAGCAACGCGATACAAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCAT 146
Db 98720 AGACAATGCACCTTATTGGTGTAAATTTGCCCTGGAATGTACAAAGAGAGTAATTCGAT 98779
QY 147 AGTTTTCACGACACTTCCAA 167
Db 98780 AGTTTTCACAGAGTCCCAA 98800

RESULT 14
AL354926/c
LOCUS Human DNA sequence from clone RP1-216J23 on chromosome 6, complete
DEFINITION sequence.
ACCESSION AL354926
VERSION AL354926.17 GI:22474401
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 163140)
AUTHORS Lawlor, S.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 23, 2002 this sequence version replaced gi:11875884.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the

* be preserved.
1 1691: contig of 1691 bp in length
1692 1791: gap of unknown length
1792 3076: contig of 1285 bp in length
3077 3176: gap of unknown length
3177 4631: contig of 1455 bp in length
4632 4731: gap of unknown length
4732 6085: contig of 1354 bp in length
6086 6185: gap of unknown length
6186 7258: contig of 1073 bp in length
7259 7358: gap of unknown length
7359 8885: contig of 1527 bp in length
8886 8985: gap of unknown length
8986 10497: contig of 1512 bp in length
10498 10597: gap of unknown length
10598 11662: contig of 1065 bp in length
11663 11762: gap of unknown length
11763 13454: contig of 1692 bp in length
13455 13554: gap of unknown length
13555 14990: contig of 1436 bp in length
14991 15090: gap of unknown length
15091 16735: contig of 1645 bp in length
16736 16835: gap of unknown length
16836 18807: contig of 1972 bp in length
18808 18907: gap of unknown length
18908 20183: contig of 1276 bp in length
20184 20283: gap of unknown length
20284 22460: contig of 2177 bp in length
22461 22560: gap of unknown length
22561 24886: contig of 2326 bp in length
24887 24986: gap of unknown length
24987 26314: contig of 1328 bp in length
26315 26414: gap of unknown length
26415 27497: contig of 1083 bp in length
27498 27597: gap of unknown length
27598 30428: contig of 2831 bp in length
30429 30528: gap of unknown length
30529 32142: contig of 1614 bp in length
32143 32242: gap of unknown length
32243 34104: contig of 1862 bp in length
34105 34204: gap of unknown length
34205 35970: contig of 1766 bp in length
35971 36070: gap of unknown length
36071 37940: contig of 1870 bp in length
37941 38040: gap of unknown length
38041 40597: contig of 2557 bp in length
40598 40697: gap of unknown length
40698 41901: contig of 1204 bp in length
41902 44468: contig of 2467 bp in length
42002 44568: gap of unknown length
44469 47391: contig of 2823 bp in length
44569 47491: gap of unknown length
47392 49980: contig of 2489 bp in length
47492 50080: gap of unknown length
49981 52156: contig of 2076 bp in length
50081 52256: gap of unknown length
52157 54625: contig of 2369 bp in length
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54626 57650: contig of 2925 bp in length
54726 57750: gap of unknown length
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61352 64463: contig of 3112 bp in length
64464 64563: gap of unknown length
64564 68139: contig of 3576 bp in length
68140 68239: gap of unknown length
68240 73090: contig of 4851 bp in length
73091 73190: gap of unknown length
73191 77708: contig of 4518 bp in length
77709 77808: gap of unknown length
77809 82473: contig of 4665 bp in length
82474 82573: gap of unknown length

* 82574 89213: contig of 6640 bp in length
* 89214 89313: gap of unknown length
* 89314 96070: contig of 6757 bp in length
* 96071 96170: gap of unknown length
* 96171 103215: contig of 7045 bp in length
* 103216 103315: gap of unknown length
* 103316 108994: contig of 5679 bp in length
* 108995 109094: gap of unknown length
* 109095 117663: contig of 8569 bp in length
* 117664 117763: gap of unknown length
* 117764 125157: contig of 7394 bp in length
* 125158 125257: gap of unknown length
* 125258 133937: contig of 8680 bp in length
* 133938 134037: gap of unknown length
* 134038 144424: contig of 10387 bp in length
* 144425 144524: gap of unknown length
* 144525 154872: contig of 10348 bp in length
* 154873 154972: gap of unknown length
* 154973 169242: contig of 14270 bp in length.

FEATURES
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1..169242
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-363J1"

BASE COUNT 48196 a 29816 c 28876 g 47557 t 14797 others
ORIGIN

Query Match 16.3%; Score 33.6; DB 2; Length 169242;
Best Local Similarity 59.4%; Pred. No. 9.1;
Matches 57; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 28 AGTTCCTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGGACAGGATAATAGAACTA 87
|||||
Db 124344 AGTTCCTGGCAAGTTTCTTGCAATCGCTGTTTACTACAAGTTGAGCTCAACAATGCTA 124403
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QY 88 AGCAACCGCATACAAATTTGGTGGATTGGCAACAAA 123
|||||
Db 124404 TGTAAGGCAACCAATATATTTGTGTTGTTAACAAA 124439
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RESULT 16
AF100673/c

LOCUS AF100673 34122 bp DNA linear INV 29-MAY-2002
DEFINITION Caenorhabditis elegans cosmid Y66H1B, complete sequence.
ACCESSION AF100673
VERSION AF100673.1 GI:3801001
KEYWORDS HTG.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis..

REFERENCE 1 (bases 1 to 34122)
AUTHORS Waterston,R.
TITLE Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
JOURNAL Science 282 (5396), 2012-2018 (1998)
MEDLINE 99069613
PUBMED 9851916

REFERENCE 2 (bases 1 to 34122)
AUTHORS Clarke,K. and Wohldmann,P.
TITLE The sequence of C. elegans cosmid Y66H1B
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 34122)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 4 (bases 1 to 34122)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA

REFERENCE	AUTHORS	TITLE	JOURNAL
1
2
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5 (bases 1 to 34122)
Waterston,R.
Direct Submission
Submitted (29-MAY-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
Submitted by:

COMMENT

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality ≥ 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.

For a graphical representation of this cosmid sequence and its analysis see:

<http://www.wormbase.org/db/seq/sequence?name=Y66H1B;class=Sequence>

NEIGHBORING COSMID INFORMATION

The 5' cosmid is F18F11, 200 bp overlap; the 3' cosmid is T07A9, 200 bp overlap. Actual end of this cosmid is at base position 8178 of W03G1.

NOTES:

Coding sequences below are the result of integration and manual review of the following data : computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFeome cloning project (<http://worfdb.dfci.harvard.edu/>), similarity to other proteins from BlastX analyses (<http://blast.wustl.edu/>), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

FEATURES

source

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/strain="Bristol N2"
/db_xref="taxon:6239"
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/gene="Y66H1B.1"
/note="for a graphical representation of this gene see:
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gene

CDS

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IDNLPIDISPGDMLFIGAIDRENMGSNEVLTVTASDSEGEKRSASATVTIRVKQRY
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EPHHEVFASVTVTVIDVNDNAPVHNTDILTHLSIEEDAQVGQVTVLVISDSDEGGVQ
KTEIDVNSTLFRADSKLVTASLKGHAGORICSTVTDVGGLRATSPCYCTVYPA
KNTHHNVLITPQKNSIHYFDENIVDEYDLKKVKLEEDGIGNVTFLRDMFEKDKWQM
FTIGEINGSLHARQAFDEKKTVHEIKILACRINNCTSHLFIISVDRDNDNCMPFKQK
DVLRLTVLENEKGKROVRIPAALSDSFHSDNTKVCYTTDTPLFFSDPTLPLFTNSS
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VQGHVTTGSHILTVQATDLDREDEGLKYSIRGFVRSPSHSFVAESPISIDKSTGELS
ATEILKSSYSFTVWTDGAGHEDTASVIVSVTYAQOTELVFDPAPFELIMKNEKTA
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yk155h4.3, CEESR11F, yk7g7.5, yk9c12.5, yk18f8.5,
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yk420e9.5, yk524c6.5"
/codon start=1
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/protein id="AAC68999.1"
/db_xref="GI:3801003"
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GPAKESRIQDRNGKCSVEYVAKAPGDYEMAIKFGKDEQKEHVKGSPFKAVVDYKKD
PSQJISGLDQPNRYLNQFVIVDITSKTKDLPVKATVPDFAQLQPVVRSRSPSNPRH
HNVRFPVSGKPNVSIPIETIYDGLKIDKLVLPVEPEPQLIKILHKKKDSLTPTPI
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DHVEYEAIGKLEYEROAERAKVWKEKEDVDVKYQKFNVRDLGQYQPKDLBAIVMP
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VGDASKVEVSGGKAGITLQANELLVDTSKAGYGLSVSVQGPSKAELTCKEVKSGSL
IKVLYTPTPEGVYAIATKPADHHVKDSPLTVQCTGKSAGRVIOITIQKDVQEHGICLPD
QESHFLKLLNTSPMDITARLMDPKGHTDDIEMRDLGGQYQLKFTPKMEGHTLSVM
YKDAHLVNGSPFQNTVSGFSEGGAKHVRAAGQGVVGTGTGFNAFNIYHREAGVGAVAV
TIEGPSKATLEFKDNDGNCHVDYKAVTPGYYVAVKFNQDHIIPDSFPKVIYAPATGE
VRKLEAQFHQGIIPAGKAFFTVTLTHRAKGHLEAKVVTNNVEDTIDIVIEDGESY
AMRVFVKETGNHFIHTVLDGAPMRESPFLRVGGKDLCDPTAISASDGLVKGTGTQK
CEFRVINTANAGALITVQMDGPSKATLDAYELEKYKVRTYPTLAPGSYFAVKYNGIH
APGSPFKIPVEGKELGGNGYNETHVKIDIAVAKTSKGTAVVPEYQGDAAKVTAKGAG
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23696..24231,24532..24808,24850..25412,25459..25632,
26482..26653,26702..26815,26865..26900))
/gene="Y66H1B.3"
/note="contains similarity to the 24 x 96 aa approximate
repeats found in human filamin (GB:L44140); coded for by
the following C. elegans cDNAs: yk363d12.5, yk348h4.3,
yk348h4.5, yk356g8.3, yk363d12.3, yk356g8.5"
/codon_start=1
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Query Match 16.2%; Score 33.4; DB 3; Length 34122;
Best Local Similarity 58.6%; Pred. No. 9.9;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 40 ATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACGCGATA 99
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Db 17600 ATTTCCAGAAATATACATTATCTAGTGAATGAAGAGAGAGAGATAAACAACAACA 17541
QY 100 CAATTTGGTGGATTGGCAACAACTTCTCTGTGACTAAC 138
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Db 17540 CAAGAAGATGTTATTGTGAAGAGAGTCTCTCTCTCAC 17502

RESULT 17
U50192
LOCUS U50192 9056 bp DNA linear INV 23-MAY-2002
DEFINITION Caenorhabditis elegans cosmid T23B7, complete sequence.
ACCESSION U50192
VERSION U50192.1 GI:1213531
KEYWORDS HTG.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 9056)
Waterston,R.

Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)

99069613
9851916
2 (bases 1 to 9056)
Pauley,A.

The sequence of C. elegans cosmid T23B7
Unpublished (2001)
3 (bases 1 to 9056)
Waterston,R.

Direct Submission
Submitted (28-FEB-1996) Robert Waterston
4 (bases 1 to 9056)
Waterston,R.

Direct Submission
Submitted (23-MAY-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA

Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63110, USA, and

Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted: all
regions were double stranded, sequenced with an alternate chemistry
or covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by sequence from
more than one ml3 subclone.

For a graphical representation of this cosmid sequence and its
analysis see:
http://www.wormbase.org/db/seq/sequence?name=T23B7;class=Sequence

NEIGHBORING COSMID INFORMATION

The 5' cosmid is C33F10, 200 bp overlap; the 3' cosmid is F11G11,
200 bp overlap. Actual start of this cosmid is at base position
28965 of C33F10; actual end is at 12575 of F11G11.

NOTES:

Coding sequences below are the result of integration and manual
review of the following data: computer analysis using the program
Genefinder (P. Green and L. Hillier, personal communication), the
large scale EST projects of Yuji Kohara
(http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C.
elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/),
similarity to other proteins from BlastX analyses
(http://blast.wustl.edu/), sequence conservation with C. briggsae
using Jim Kent's WABA alignment program (Genome Research
10:1115-1125, 2000), individual C. elegans GenBank submissions,
and personal communications with C. elegans research groups.
are predicted using the program tRNAscan-SE (Lowe, T.M. and
Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

FEATURES
source

1..9056
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="II"
/clone="T23B7"
1153..1368
/gene="T23B7.1"

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/note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=T23B7.1;class
=Sequence"
1153..1368
/gene="T23B7.1"

CDS

/note="coded for by the following C. elegans cDNAs:
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/codon_start=1
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/protein_id="AAA91245.1"
/db_xref="GI:1213532"
/translation="MADKSAVMGAGGYGSGYMGNSASSGYAREDYAQGGNGGQQQQQ
NQSGGNTNPGGVQFKARTDQSCYLGP"
BASE COUNT 2739 a 1738 c 1459 g 3120 t

ORIGIN

Query Match 16.0%; Score 33; DB 3; Length 9056;
Best Local Similarity 49.2%; Pred. No. 13;
Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 28 AGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTA 87
|||||
Db 2567 AATTATTATCCGTTCCGACTCAAAATTAGATTAAATCAATTACCAGCCTCCAGCATTTTC 2626

```

QY      88  ACACGCGATACAAATTTGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATA 147
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Db      2627  AGCATTTTCCAAATTTGTTCCCTTATTTTCCCTTAAACTTGCTGTGACATCATTTTCGTAA 2686
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      148  GTTTTTCAGGACACTTCCAGGACGCCATACCGAACAAAGCAAGGTGTATTATTCCT 204
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      2687  CATTTTCCAGTAAGATCCCGAAATCATAGCGAACAGTGAAAAATGTTACAGTGCT 2743
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 18
AC015606/c
LOCUS      AC015606                      68850 bp    DNA      linear      HTG 13-JUL-2000
DEFINITION Homo sapiens clone RP11-45E12, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC015606
VERSION    AC015606.2  GI:9103689
KEYWORDS  HTG; HTGS_PHASE0.
SOURCE    Homo sapiens.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 68850)
AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
TITLE     Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
JOURNAL   Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
REFERENCE Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
           Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
           Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
           Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
           Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
           McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
           Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
           Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
           Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
           Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
           Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
           Direct Submission
SUBMITTED (17-NOV-1999) Whitehead Institute/MIT Center for Genome
RESEARCH, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6447081.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1137
Center clone name: 45_E_12
-----
* NOTE: This record contains 71 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 887: contig of 887 bp in length
* 888 987: gap of 100 bp
* 988 1854: contig of 867 bp in length
* 1855 1954: gap of 100 bp
* 1955 2812: contig of 858 bp in length
* 2813 2912: gap of 100 bp

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* 2913 3781: contig of 869 bp in length
* 3782 3881: gap of 100 bp
* 3882 4749: contig of 868 bp in length
* 4750 4849: gap of 100 bp
* 4850 5710: contig of 861 bp in length
* 5711 5810: gap of 100 bp
* 5811 6691: contig of 881 bp in length
* 6692 6791: gap of 100 bp
* 6792 7650: contig of 859 bp in length
* 7651 7750: gap of 100 bp
* 7751 8617: contig of 867 bp in length
* 8618 8717: gap of 100 bp
* 8718 9584: contig of 867 bp in length
* 9585 9684: gap of 100 bp
* 9685 10550: contig of 866 bp in length
* 10551 10650: gap of 100 bp
* 10651 11522: contig of 872 bp in length
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* 11623 12498: contig of 876 bp in length
* 12499 12598: gap of 100 bp
* 12599 13465: contig of 867 bp in length
* 13466 13565: gap of 100 bp
* 13566 14444: contig of 879 bp in length
* 14445 14544: gap of 100 bp
* 14545 15414: contig of 870 bp in length
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* 18413 19291: contig of 879 bp in length
* 19292 19391: gap of 100 bp
* 19392 20269: contig of 878 bp in length
* 20270 20369: gap of 100 bp
* 20370 21234: contig of 865 bp in length
* 21235 21334: gap of 100 bp
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* 22203 22302: gap of 100 bp
* 22303 23183: contig of 881 bp in length
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* 27174 28041: contig of 868 bp in length
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* 29013 29112: gap of 100 bp
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* 31073 31940: contig of 868 bp in length
* 31941 32040: gap of 100 bp
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* 32912 33011: gap of 100 bp
* 33012 33890: contig of 879 bp in length
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* 35871 35970: gap of 100 bp
* 35971 36839: contig of 869 bp in length
* 36840 36939: gap of 100 bp
* 36940 37806: contig of 867 bp in length
* 37807 37906: gap of 100 bp
* 37907 38773: contig of 867 bp in length

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COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GQPZ
Center clone name: CH230-267P11
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 46755 bases at least Q40
Consensus quality: 53605 bases at least Q30
Consensus quality: 58794 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 43 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1029 1128: gap of unknown length
1129 2179: contig of 1051 bp in length
2180 2279: gap of unknown length
2280 3727: contig of 1448 bp in length
3728 3827: gap of unknown length
3828 5211: contig of 1384 bp in length
5212 5311: gap of unknown length
5312 6688: contig of 1377 bp in length
6689 6789: gap of unknown length
6789 7919: contig of 1130 bp in length
7919 8018: gap of unknown length
8018 9549: contig of 1531 bp in length
9550 9649: gap of unknown length
9650 10843: contig of 1194 bp in length
10844 10943: gap of unknown length
10944 12210: contig of 1267 bp in length
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12311 13726: contig of 1416 bp in length
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17893 19114: contig of 1222 bp in length
19115 19214: gap of unknown length
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20643 20743: gap of unknown length
20743 21851: contig of 1109 bp in length
21852 21951: gap of unknown length
21952 22953: contig of 1002 bp in length
22954 23053: gap of unknown length
23054 25122: contig of 2069 bp in length
25123 25222: gap of unknown length
25223 26239: contig of 1017 bp in length
26240 26339: gap of unknown length
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28536 30072: contig of 1437 bp in length
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31385 32603: contig of 1219 bp in length
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32704 34134: contig of 1431 bp in length

* 34135 34234: gap of unknown length
* 34235 36423: contig of 2189 bp in length
* 36424 36523: gap of unknown length
* 36524 38469: contig of 1946 bp in length
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* 41320 41419: gap of unknown length
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* 43188 43287: gap of unknown length
* 43288 45114: contig of 1827 bp in length
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FEATURES

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/db_xref="taxon:10116"
/clone="CH230-267P11"

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Best Local Similarity 54.5%; Pred. No. 14;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0

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|||||
QY 136 AACAGGTCCATAGTTTTCACGACACTTCCAAAGGACGCCATACCGAACAAGCAAGGTGT 195
|||||
Db 62377 AAGAGATTGTTAGTTTAAAGGATGGCCAATGATGGCATCTTCAAAATATCAGGTTT 62318
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Db 62317 T 62317

RESULT 20

AC110319
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DEFINITION AC110319 Rattus norvegicus clone CH230-234D19, *** SEQUENCING IN PROGRESS
ACCESSION AC110319
VERSION AC110319.3 GI:21736734
KEYWORDS HTG; HTGS PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

AC110319 174900 bp DNA linear HTG 13-JUL-2002

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 174900)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaral, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B.,
Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozdo, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Umanis, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 174900)
Worley, K.C.

Direct Submission
Submitted (11-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 174900)
Worley, K.C.

Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jul 12, 2002 this sequence version replaced gi:18846430.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GOHK
Center clone name: CH230-234D19
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 94694 bases at least Q40
Consensus quality: 99249 bases at least Q30

Consensus quality: 103736 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 79 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1048: contig of 1048 bp in length
1049 1148: gap of unknown length
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2413 2512: gap of unknown length
2513 3550: contig of 1038 bp in length
3551 3650: gap of unknown length
3651 4992: contig of 1342 bp in length
4993 5092: gap of unknown length
5093 6320: contig of 1228 bp in length
6321 6420: gap of unknown length
6421 7606: contig of 1186 bp in length
7607 7706: gap of unknown length
7707 8744: contig of 1038 bp in length
8745 8845: gap of unknown length
8845 9951: contig of 1107 bp in length
9952 10051: gap of unknown length
10052 11218: contig of 1167 bp in length
11219 12449: contig of 1131 bp in length
12450 12549: gap of unknown length
12550 13666: contig of 1117 bp in length
13667 13766: gap of unknown length
13767 15045: contig of 1279 bp in length
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15146 16249: contig of 1104 bp in length
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17490 17589: gap of unknown length
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21202 22551: contig of 1350 bp in length
22552 22651: gap of unknown length
22652 23858: contig of 1207 bp in length
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25442 26743: contig of 1302 bp in length
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26844 28098: contig of 1255 bp in length
28099 28198: gap of unknown length
28199 29533: contig of 1335 bp in length
29534 29633: gap of unknown length
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30930 31029: gap of unknown length
31030 32335: contig of 1306 bp in length
32336 32435: gap of unknown length
32436 33893: contig of 1458 bp in length
33894 33993: gap of unknown length
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35354 35453: gap of unknown length
35454 37134: contig of 1681 bp in length
37135 37234: gap of unknown length
37235 38583: contig of 1349 bp in length
38584 38683: gap of unknown length
38684 40080: contig of 1397 bp in length
40081 40180: gap of unknown length
40181 41961: contig of 1781 bp in length

* 41962 42061: gap of unknown length
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* 66220 68675: contig of 2456 bp in length
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* 73301 73400: gap of unknown length
* 73401 75244: contig of 1844 bp in length
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* 77270 77369: gap of unknown length
* 77370 79197: contig of 1828 bp in length
* 79198 79297: gap of unknown length
* 79298 82051: contig of 2754 bp in length
* 82052 82151: gap of unknown length
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Query Match 16.0%; Score 33; DB 2; Length 174900;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 76 ATAATAGAACTAAGCAACGCCGATACAAATTTGGTGGATTGGCAACAACTTCCTGTGACT 135
Db 88698 ATAATTACCAATGTTCTTTTAAAACTATGCTGTCTGTCCACCCATGTGTATGTCAT 88757
QY 136 AACAGGTCCATAGTTTTTCACGACACTTCCAGGACGCCATACCGAACAAAGCAAGGTGT 195
Db 88758 AAGAGATTGTTAGTTTTTAAAGGGATGGCCAAATGATGGCATCTTCAAATATCAGGTTT 88817
QY 196 T 196
Db 88818 T 88818

RESULT 21
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LOCUS AC090127 212404 bp DNA linear ROD 27-APR-2002
DEFINITION Mus musculus chromosome 6, clone RP23-128D23, complete sequence.
ACCESSION AC090127
VERSION AC090127.11 GI:20330898
KEYWORDS HTG.
SOURCE Mus musculus.
ORGANISM Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 212404)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,
Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 212404)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (26-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 212404)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,

SOURCE
ORGANISM

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS
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house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 213265)

Birren,B., Nusbaum,C. and Lander,E.

Mus musculus, clone RP23-132J19

Unpublished

2 (bases 1 to 213265)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
McClean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

TITLE	JOURNAL	REFERENCE	AUTHORS
1. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.
2. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.
3. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.
4. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.
5. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.
6. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.
7. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.
8. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.
9. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.
10. The effect of the concentration of the solution on the rate of the reaction	Journal of Physical Chemistry	1950	Smith, J. D.

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FEATURES
  Location/Qualifiers
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      source
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misc feature

misc feature

misc feature

misc feature

misc feature

mid feature

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2
7
4
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4

0
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0
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3

4

U

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BASE COUNT      61646 a 46010 c 45341 g
VECTOR_SIDE:right
ORIGIN
900 others
59368 t
45341 g
46010 c
61646 a

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Query Match 16.0%; Score 33; DB 2; Length 213265;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 66: Conservative 0; Mismatches 55; Indels 0

QY 31 TCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACAATAAGC 90
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Db 125005 TCATACTCAATTGAGAGTTTAGTGATGTGCCATTCTTAAACAAGACAAAAGGGGCAAC 125064

gene VRENELTYQFORWQNHVTRILESSEGIKLPKPSDTLVSDRLHQAQNDVTAQRWVLTE
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/protein_id="AAG57984.1"
/db_xref="GI:12517370"

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/gene="Z4193"
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molecules: Protein, peptide secretion"
/note="Residues 2 to 102 of 111 are 31.68 pct identical to
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enterica]"
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/transl_table=11
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/protein_id="AAG57985.1"
/db_xref="GI:12517371"

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CDS KYNGRSQEN"
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complement(3697. .5016)
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/function="putative transport; Transport of large
molecules: Protein, peptide secretion"
/note="Residues 10 to 396 of 439 are 63.30 pct identical
to residues 1 to 386 of 432 from GenPept 118 :
gi|497222|gb|AAA74038.1| (U08279) invC [Salmonella
typhimurium]"
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CVLVYATSDFSVDRCAALMATVAEYFRDRGKRVFLPDSMTRYARALRDMKLAAG
EPARRGYPASVFDLSPLRLRPGPTLKGSIETEFYVLLGEDESDPLGDEIRSLDG
HIYLSRLAQGGHYPAIDVLKSVSRVFGQVTEKRDNAARVRKNLTTLLEDLQVFIDL
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/function="putative transport; Transport of large
molecules: Protein, peptide secretion"
/note="Residues 1 to 686 of 686 are 64.00 pct identical to
residues 1 to 685 of 685 from GenPept 118 :
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Query Match 15.9%; Score 32.8; DB 1; Length 10875;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 82; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 34 TGGTCAATTTCCAGGACACAGATGATTCTGGTCCAGAACAGGATAATAGCAAC 93
Db 8002 TGGCCAATTTTCTGGACGAGAGAAATATGTCTCTGGAAGACCAGCCCAATAGAAAAACCG 7943

QY 94 GCGATACAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTT 153
Db 7942 ACAAAAGTTATGGAGCGCTTAAGGCTGCAACTACCCATGACTATGAAGTGTATAGCTTTG 7883
QY 154 CACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTA 197
Db 7882 CTAAAAAATATTCCAGATCAAAGCGATCTGGTAGTTGTGTTA 7839

RESULT 24
AR204270/c 16950 bp DNA linear PAT 20-JUN-2002
LOCUS AR204270
DEFINITION Sequence 166 from patent US 6365723.
ACCESSION AR204270
VERSION AR204270.1 GI:21500877
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16950)
AUTHORS Blattner,F.R., Burland,V., Perna,N.T., Plunkett,G. and Welch,R.
TITLE Sequences of E. coli O157
JOURNAL Patent: US 6365723-A 166 02-APR-2002;
FEATURES Location/Qualifiers
source 1..16950
/organism="unknown"

BASE COUNT 5138 a 3505 c 2750 g 5557 t
ORIGIN

Query Match 15.9%; Score 32.8; DB 6; Length 16950;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 82; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 34 TGGTCAATTTCCAGGACACAGATGATTCTGGTCCAGAACAGGATAATAGCAAC 93
Db 13213 TGGCCAATTTTCTGGACGAGAGAAATATGTCTGGAAGACCAGCCCAATAGAAAAACCG 13154

QY 94 GCGATACAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTT 153
Db 13153 ACAAAAGTTATGGAGCGCTTAAGGCTGCAACTACCCATGACTATGAAGTGTATAGCTTTG 13094

QY 154 CACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTA 197
Db 13093 CTAAAAAATATTCCAGATCAAAGCGATCTGGTAGTTGTGTTA 13050

RESULT 25
AC108788 75344 bp DNA linear HTG 14-JUN-2002
LOCUS AC108788
DEFINITION Mus musculus clone RP24-141E2, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC108788
VERSION AC108788.2 GI:21426227
KEYWORDS HTG; HTGS_PHASE0.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 75344)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP24-141E2
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 75344)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Chazaro,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,

Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

AUTHORS

3 (bases 1 to 75344)
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faroo, S., Ferreira, P., Fitzgerald, M., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Jun 14, 2002 this sequence version replaced gi:18450046.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L19501

Center clone name: 141_E_2

* NOTE: This record contains 89 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

* 1 722: contig of 722 bp in length

* 723 822: gap of 100 bp

* 823 1565: contig of 743 bp in length

* 1566 1665: gap of 100 bp

* 1666 2441: contig of 776 bp in length

* 2442 2541: gap of 100 bp

* 2542 3310: contig of 769 bp in length

* 3311 3410: gap of 100 bp

*

* 3411 4082: contig of 672 bp in length
* 4083 4182: gap of 100 bp
* 4183 4917: contig of 735 bp in length
* 4918 5017: gap of 100 bp
* 5018 5762: contig of 745 bp in length
* 5763 5862: gap of 100 bp
* 5863 6616: contig of 754 bp in length
* 6617 6716: gap of 100 bp
* 6717 7472: contig of 756 bp in length
* 7473 7572: gap of 100 bp
* 7573 8335: contig of 763 bp in length
* 8336 8435: gap of 100 bp
* 8436 9188: contig of 753 bp in length
* 9189 9288: gap of 100 bp
* 9289 10046: contig of 758 bp in length
* 10047 10146: gap of 100 bp
* 10147 10872: contig of 726 bp in length
* 10873 10972: gap of 100 bp
* 10973 11739: contig of 767 bp in length
* 11740 11839: gap of 100 bp
* 11840 12537: contig of 698 bp in length
* 12538 12637: gap of 100 bp
* 12638 13389: contig of 752 bp in length
* 13390 13489: gap of 100 bp
* 13490 14209: contig of 720 bp in length
* 14210 14309: gap of 100 bp
* 14310 15020: contig of 711 bp in length
* 15021 15120: gap of 100 bp
* 15121 15865: contig of 745 bp in length
* 15866 15965: gap of 100 bp
* 15966 16727: contig of 762 bp in length
* 16728 16827: gap of 100 bp
* 16828 17593: contig of 766 bp in length
* 17594 17693: gap of 100 bp
* 17694 18456: contig of 763 bp in length
* 18457 18556: gap of 100 bp
* 18557 19334: contig of 778 bp in length
* 19335 19434: gap of 100 bp
* 19435 20207: contig of 773 bp in length
* 20208 20307: gap of 100 bp
* 20308 21034: contig of 727 bp in length
* 21035 21134: gap of 100 bp
* 21135 21895: contig of 761 bp in length
* 21896 21995: gap of 100 bp
* 21996 22765: contig of 770 bp in length
* 22766 22865: gap of 100 bp
* 22866 23579: contig of 714 bp in length
* 23580 23679: gap of 100 bp
* 23680 24411: contig of 732 bp in length
* 24412 24511: gap of 100 bp
* 24512 25261: contig of 750 bp in length
* 25262 25361: gap of 100 bp
* 25362 26119: contig of 758 bp in length
* 26120 26219: gap of 100 bp
* 26220 26979: contig of 760 bp in length
* 26980 27079: gap of 100 bp
* 27080 27844: contig of 765 bp in length
* 27845 27944: gap of 100 bp
* 27945 28708: contig of 764 bp in length
* 28709 28808: gap of 100 bp
* 28809 29532: contig of 724 bp in length
* 29533 29632: gap of 100 bp
* 29633 30399: contig of 767 bp in length
* 30400 30499: gap of 100 bp
* 30500 31252: contig of 753 bp in length
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* 31353 32078: contig of 726 bp in length
* 32079 32178: gap of 100 bp
* 32179 32906: contig of 728 bp in length
* 32907 33006: gap of 100 bp
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repeat_region 9835. .10129
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repeat_region 13308. .13601
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Query Match 15.8%; Score 32.6; DB 9; Length 90422;
Best Local Similarity 57.3%; Pred. No. 19;
Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 19 ACGTATACGAGTTCTTGGTCAATTTCCAGCACACAGATGATTCGGTCCCAAGAACAGGATA 78
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Db 47572 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGGTAA 47631
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QY 79 ATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACA 121
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Db 47632 GTGCAGGAAACAAGAAATATTTTCAGAGTATAGTCAAAA 47674
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RESULT 27
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LOCUS AC079746 131133 bp DNA linear HTG 12-JAN-2001
DEFINITION Homo sapiens chromosome 7 clone CTD-235302, WORKING DRAFT SEQUENCE
19 unordered pieces.
ACCESSION AC079746
VERSION AC079746.2 GI:12084089
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 131133)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 131133)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jan 12, 2001 this sequence version replaced gi:10047925.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

3 (bases 1 to 159480)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnuez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (01-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 1, 2001 this sequence version replaced gi:12658133.

COMMENT

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L6094

Center clone name: 713_C_1

FEATURES

source

Location/Qualifiers

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/clone="RP11-713C1"
/clone_lib="RPC1-11 Human Male BAC"

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Best Local Similarity 51.7%; Pred. No. 19;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 26 CGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATAATAGAAC 85
Db 80585 CCAACTCTGGGTCAATTTGAGTGCACAAATAAAATATTAACCCAACTATAAAATAATA 80526

QY 86 TAAGCAACGCGATACAATTTGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCCA 145
Db 80525 TCCATGAGTCTATACAGATATAGATGATTTTAAATAATAATTTGGAGTAAAGGGACA 80466

QY 146 TAGTTTTCAGCACACTTCCAAAG 168
Db 80465 AATCTGTGAAGACAATTCCAAG 80443
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RESULT 29
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LOCUS              AC090770              168406 bp      DNA      linear      HTG 23-MAY-2001
DEFINITION         Homo sapiens chromosome 18 clone RP11-82109 map 18, WORKING DRAFT
SEQUENCE           SEQUENCE, 5 unordered pieces.
AC090770
AC090770.2         GI:14190727
KEYWORDS            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE              Homo sapiens.
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE           1 (bases 1 to 168406)
AUTHORS             Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
TITLE               Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,
JOURNAL             Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
REFERENCE           Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
AUTHORS             Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
TITLE               2 (bases 1 to 168406)
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Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,
Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Pollara,V., Rogov,P., Roman,J., Rosetti,M.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 23, 2001 this sequence version replaced gi:13270639.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12573
Center clone name: 821_O_9
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 165824 bases at least Q40
Consensus quality: 166641 bases at least Q30
Consensus quality: 167254 bases at least Q20
Insert size: 170000; agarose-fp
Quality coverage: 10.4 in Q20 bases; agarose-fp
Quality coverage: 10.5 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 5990: contig of 5990 bp in length
* 5991 6090: gap of 100 bp
* 6091 13492: contig of 7402 bp in length
* 13493 13592: gap of 100 bp
* 13593 22513: contig of 8921 bp in length
* 22514 22613: gap of 100 bp
* 22614 56584: contig of 33971 bp in length
* 56585 56685: gap of 100 bp
* 56685 168406: contig of 111722 bp in length.
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/db_xref="taxon:9606"
/chromosome="18"
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/clone="RP11-82109"
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1. 5990
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Query Match      15.8%; Score 32.6; DB 2; Length 170337;
Best Local Similarity 51.7%; Pred. No. 19;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 26 CGACTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAAC 85
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QY 86 TAACCAACGCCATACAAATTTGGGTGGATTGGCAACAAACTTCCTGTGCTAACAGGTCCA 145
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Db 69958 TCCATGAGTCTATACAGATATAGATGATTTTAAAAATAAATAATTGGAGTAAAGGGACA 69899

QY 146 TAGTTTTCAGCACACTTCCAAG 168
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RESULT 31
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LOCUS          AC027216          170843 bp      DNA      linear      PRI 11-DEC-2001
DEFINITION    Homo sapiens chromosome 18, clone RP11-440L16, complete sequence.
ACCESSION     AC027216
VERSION       AC027216.6  GI:17488727
KEYWORDS      HTG.
SOURCE        Homo sapiens.
ORGANISM      Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 170843)
AUTHORS       Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE         Homo sapiens chromosome 18, clone RP11-440L16
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 170843)
AUTHORS       Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
               Anderson,S., Baldwin,J., Barna,N., Bastien,V., Boguslavskiy,L., Boda,F.,
               Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
               Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
               Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
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               Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
               Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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               Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
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               Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
               Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 170843)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Farooq,S., Ferreira,P.,
FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S.,
Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
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Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T.,
Lehoczkyl,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (03-JUL-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 170843)

TITLE
JOURNALREFERENCE
AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Farooq,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczkyl,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (11-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 11, 2001 this sequence version replaced gi:14589638.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE
JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L8189
Center clone name: 440_L16

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1120..1142
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repeat_region
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Center project name: chr-7
Center clone name: RP11-738B7 (djs722)
----- Summary Statistics -----
Assembly program: Phrap; version 0.990319
Consensus quality: 176414 bases at least Q40
Consensus quality: 176547 bases at least Q30
Consensus quality: 176562 bases at least Q20
Insert size: 176562; sum-of-contigs
Quality coverage: 12.0x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-448A19 (UWGC:djs705) AC078846 58194-bp overlap
3': RP11-437L1 (UWGC:djs723) AC084865 98271-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
8696	8837	9894	9869	5769	5639
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3072	3060	512	<800	6151	6222
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4548	4514	732	772	6476	6481
1422	1494	300	<800	89	<800
10713	10620	261	<800	2525	2559
7612	7664	3459	3373	681	<800
1478	1494	597	<800	1924	1902
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FEATURES
source

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/db_xref="taxon:9606"
/chromosome="7"

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2957	2902	1091	1115	3945	4079
4167	4235	1129	1115	4649	4766
6118	6170	2198	2282	1854	1902
7425	7499	4177	4278	7735	7953
1918	2065	24114	24615	19	<800
3930	3930	3744	3797	920	915
24765	24846	2477	2480	1950	1902
10168	10620	1254	1273	7997	7953
543	<800	7662	7831	12518	12362
587	<800	1397	1507	17895	18146
562	<800	3724	3797	2611	2728
10971	10620	1272	1273	684	<800
4315	4235	3335	3373	2714	2728
5736	5630	2806	2809	1157	1158
748	764	310	<800	5200	5136
2861	2902	777	772	1038	1041
10495	10620	9726	9869	2986	2986
7	<800	20519	20229	327	<800
		3821	3797	81	<800
		22	<800	5265	5136
		454	<800	3434	3411
		6414	6431	900	915
		907	915	34	<800
		2334	2480	470	<800
		284	<800	3878	3862
		3580	3509	3274	3411
		150	<800	8043	7953
		1262	1273	1863	1902
		5121	5107	2821	2986
		183	<800	3024	3237

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 177013)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Choristopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Foster,P., Frantz,P.,
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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Kratzson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 177013)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 177013)
Worley,K.C.
Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:17943862.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GEOZ
Center clone name: CH230-11D3
----- Summary Statistics
Sequencing vector: Plasmid:
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 113564 bases at least Q40

COMMENT

Consensus quality: 120262 bases at least Q30
Consensus quality: 127025 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 73 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1015: contig of 1015 bp in length
* 1016 1115: gap of unknown length
* 1116 2180: contig of 1065 bp in length
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* 2281 3821: contig of 1541 bp in length
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* 12156 12255: gap of unknown length
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* 17641 19310: contig of 1670 bp in length
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* 30114 31248: contig of 1135 bp in length
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* 32908 33007: gap of unknown length
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* 42188 42287: gap of unknown length
* 42288 43462: contig of 1175 bp in length
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between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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6	<800	6382	6405	2067	2040						
3758	3742	512	<800	7141	7259						
7910	8026	449	<800	2876	3002						
7475	7546	11460	11201	6256	6289						
11060	11037	6972	6952	10615	10586						
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562	<800	3813	3793	4013	3914						
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		3821	3793	5265	5138
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		9726	10019	327	<800
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FEATURES
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/chromosome="7"

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Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Db 67265 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGGTAA 67206
QY 79 ATAGAACTAAGCAACGCGATACAATTTGGGTGATTGGCAACA 121
Db 67205 GTGCAGGAAAACAAGAGAAATATTTTCAGAGTATAGTCAAAA 67163

RESULT 36
AC005872
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DEFINITION Homo sapiens chromosome 10 clone CIT987SK-113711, complete sequence.
ACCESSION AC005872
VERSION AC005872.2 GI:4314335
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
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Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

2 (bases 1 to 127049)

Worley, K.C.

Direct Submission

Submitted (03-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GNYH

Center clone name: CH230-133H8

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 70751 bases at least Q40

Consensus quality: 77839 bases at least Q30

Consensus quality: 83524 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 59 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1005: contig of 1005 bp in length

* 1006 1105: gap of unknown length

* 1106 2375: contig of 1270 bp in length

* 2376 2475: gap of unknown length

* 2476 3845: contig of 1370 bp in length

* 3846 3945: gap of unknown length

* 3946 5274: contig of 1329 bp in length

* 5275 5374: gap of unknown length

* 5375 6468: contig of 1094 bp in length

* 6469 6568: gap of unknown length

* 6569 7779: contig of 1211 bp in length

* 7780 7879: gap of unknown length

* 7880 9507: contig of 1628 bp in length

* 9508 9607: gap of unknown length

* 9608 11184: contig of 1577 bp in length

* 11185 11284: gap of unknown length

* 11285 12576: contig of 1292 bp in length

* 12577 12676: gap of unknown length

12677 14232: contig of 1556 bp in length

14233 14332: gap of unknown length

14333 15683: contig of 1351 bp in length

15684 15783: gap of unknown length

15784 17331: contig of 1548 bp in length

17332 17431: gap of unknown length

17432 18997: contig of 1466 bp in length

18998 20217: contig of 1220 bp in length

20218 20317: gap of unknown length

20318 21553: contig of 1236 bp in length

21554 21653: gap of unknown length

21654 23329: contig of 1676 bp in length

23330 23429: gap of unknown length

23430 25134: contig of 1705 bp in length

25135 26332: contig of 1098 bp in length

26333 26432: gap of unknown length

26433 28753: contig of 2321 bp in length

28754 28853: gap of unknown length

28854 30050: contig of 1197 bp in length

30051 30150: gap of unknown length

30151 31280: contig of 1130 bp in length

31281 31380: gap of unknown length

31381 32754: contig of 1374 bp in length

32755 32854: gap of unknown length

32855 34227: contig of 1373 bp in length

34228 34327: gap of unknown length

34328 35908: contig of 1581 bp in length

35909 36008: gap of unknown length

36009 37404: contig of 1396 bp in length

37405 37504: gap of unknown length

37505 39495: contig of 1991 bp in length

39496 39595: gap of unknown length

39596 41276: contig of 1681 bp in length

41277 41376: gap of unknown length

41377 42869: contig of 1493 bp in length

42870 42969: gap of unknown length

42970 44558: contig of 1589 bp in length

44559 44658: gap of unknown length

44659 46042: contig of 1384 bp in length

46043 46142: gap of unknown length

46143 48103: contig of 1961 bp in length

48104 48203: gap of unknown length

48204 49818: contig of 1615 bp in length

49819 49918: gap of unknown length

49919 51313: contig of 1395 bp in length

51314 51413: gap of unknown length

51414 53441: contig of 2028 bp in length

53442 53541: gap of unknown length

53542 55482: contig of 1941 bp in length

55483 55582: gap of unknown length

55583 57123: contig of 1541 bp in length

57124 57223: gap of unknown length

57224 58644: contig of 1421 bp in length

58645 58744: gap of unknown length

58745 60428: contig of 1684 bp in length

60429 60528: gap of unknown length

60529 61918: contig of 1390 bp in length

61919 62018: gap of unknown length

62019 63462: contig of 1444 bp in length

63463 63562: gap of unknown length

63563 65389: contig of 1827 bp in length

65390 65489: gap of unknown length

65490 67605: contig of 2116 bp in length

67606 67705: gap of unknown length

67706 69237: contig of 1532 bp in length

69238 69337: gap of unknown length

69338 71582: contig of 2245 bp in length

71583 71682: gap of unknown length

71683 73872: contig of 2190 bp in length

73873 73972: gap of unknown length

73973 76349: contig of 2377 bp in length

Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
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Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 154139)
Worley, K.C.

Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 154139)
Worley, K.C.

Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jul 10, 2002 this sequence version replaced gi:20975907.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GDS
Center clone name: CH230-9F24
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 84102 bases at least Q40
Consensus quality: 90883 bases at least Q30
Consensus quality: 96268 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

* consists of 73 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1319: contig of 1319 bp in length
* 1320: gap of unknown length
* 1420: contig of 1578 bp in length
* 2997: contig of 1578 bp in length
* 2998: gap of unknown length
* 3097: contig of 1450 bp in length
* 4547: gap of unknown length
* 4648: contig of 1181 bp in length
* 5828: gap of unknown length
* 5928: contig of 1350 bp in length
* 7278: gap of unknown length
* 7378: contig of 1327 bp in length
* 8705: gap of unknown length
* 8805: gap of unknown length
* 10379: contig of 1574 bp in length
* 10479: gap of unknown length
* 11570: contig of 1091 bp in length
* 11670: gap of unknown length
* 13216: contig of 1546 bp in length
* 13316: gap of unknown length
* 14902: contig of 1586 bp in length
* 15002: gap of unknown length
* 16037: contig of 1035 bp in length
* 16137: gap of unknown length
* 17341: contig of 1204 bp in length
* 17441: gap of unknown length
* 18649: contig of 1208 bp in length
* 18749: gap of unknown length
* 20166: gap of unknown length
* 20266: contig of 1417 bp in length
* 21753: contig of 1487 bp in length
* 21853: gap of unknown length
* 23008: contig of 1155 bp in length
* 23108: gap of unknown length
* 24903: contig of 1795 bp in length
* 25003: gap of unknown length
* 26766: contig of 1763 bp in length
* 26866: gap of unknown length
* 28363: contig of 1497 bp in length
* 28463: gap of unknown length
* 29781: contig of 1318 bp in length
* 29881: gap of unknown length
* 31265: contig of 1384 bp in length
* 31365: gap of unknown length
* 33019: contig of 1654 bp in length
* 33119: gap of unknown length
* 34327: contig of 1208 bp in length
* 34427: gap of unknown length
* 35872: contig of 1445 bp in length
* 35972: gap of unknown length
* 37574: contig of 1602 bp in length
* 37674: gap of unknown length
* 39188: contig of 1514 bp in length
* 39288: gap of unknown length
* 41702: contig of 2414 bp in length
* 41802: gap of unknown length
* 44019: contig of 2217 bp in length
* 44119: gap of unknown length
* 45597: contig of 1478 bp in length
* 45697: gap of unknown length
* 47459: contig of 1762 bp in length
* 47559: gap of unknown length
* 48952: contig of 1393 bp in length
* 49052: gap of unknown length
* 50791: contig of 1739 bp in length
* 50891: gap of unknown length
* 52432: contig of 1541 bp in length
* 52532: gap of unknown length

Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojebokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished
2 (bases 1 to 154096)
Worley, K.C.

Direct Submission

Submitted (28-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 154096)

Worley, K.C.

Direct Submission

Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 14, 2002 this sequence version replaced gi:20429742.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GVAV

Center clone name: CH230-297018

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 134322 bases at least Q40

Consensus quality: 137161 bases at least Q30

Consensus quality: 139528 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 27 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 1141: contig of 1141 bp in length

1142 1241: gap of unknown length

1242 2392: contig of 1151 bp in length

2393 2492: gap of unknown length

2493 3990: contig of 1498 bp in length

3991 4090: gap of unknown length

4091 5310: contig of 1220 bp in length

5311 5410: gap of unknown length

5411 7230: contig of 1820 bp in length

* 7231 7330: gap of unknown length
* 7331 9463: contig of 2133 bp in length
* 9464 9563: gap of unknown length
* 9564 11726: contig of 2163 bp in length
* 11727 11826: gap of unknown length
* 11827 13533: contig of 1707 bp in length
* 13534 13633: gap of unknown length
* 13634 16389: contig of 2756 bp in length
* 16390 16489: gap of unknown length
* 16490 19305: contig of 2816 bp in length
* 19306 19405: gap of unknown length
* 19406 23044: contig of 3639 bp in length
* 23045 23144: gap of unknown length
* 23145 27931: contig of 4787 bp in length
* 27932 28031: gap of unknown length
* 28032 30805: contig of 2774 bp in length
* 30806 30905: gap of unknown length
* 30906 35236: contig of 4331 bp in length
* 35237 35336: gap of unknown length
* 35337 42707: contig of 7371 bp in length
* 42708 42807: gap of unknown length
* 42809 48408: contig of 5601 bp in length
* 48409 48508: gap of unknown length
* 48509 55834: contig of 7326 bp in length
* 55835 55934: gap of unknown length
* 55935 60641: contig of 4706 bp in length
* 60641 60741: gap of unknown length
* 60741 68288: contig of 7548 bp in length
* 68289 68388: gap of unknown length
* 68389 72774: contig of 4396 bp in length
* 72775 72874: gap of unknown length
* 72875 80134: contig of 7260 bp in length
* 80135 80234: gap of unknown length
* 80235 85591: contig of 5357 bp in length
* 85592 85692: gap of unknown length
* 85692 92657: contig of 6966 bp in length
* 92658 92757: gap of unknown length
* 92758 102293: contig of 9536 bp in length
* 102294 102393: gap of unknown length
* 102394 118633: contig of 16240 bp in length
* 118634 118733: gap of unknown length
* 118734 130814: contig of 12081 bp in length
* 130815 130914: gap of unknown length
* 130915 154096: contig of 23182 bp in length.

FEATURES

source

1..154096

/organism="Rattus norvegicus"

/db_xref="taxon:10116"

/clone="CH230-297018"

BASE COUNT 44409 a 28305 c 29844 g 46270 t 5268 others

ORIGIN

Query Match 15.5%; Score 32; DB 2; Length 154096;

Best Local Similarity 48.4%; Pred. No. 30;

Matches 89; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 22 TATACGAGTTCTTGGTCAATTTCAGGACACACATGATTCGGTCCAGAAACAGGATAATA 81

Db 500 TACAGGAGTGTGACACACAGGCCAACAGGGAGGTCAAGCCACTGTCTCAGACAGCAAGT 559

QY 82 GAACTAAGCAACGGGATACAAATTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGG 141

Db 560 CAAGCTAACACCAGGGACAAATGTATGGTGAGGCAAGCAAGGAGATTAAAGCAACAGA 619

QY 142 TCCATAGTTTTTCACGACACTTCCAGGAGGCCATACCGCAACAAAGCAAGTGTATTAT 201

Db 620 ATCTAAGACTACCAGGCATCTTCAGAGCACAGTACTCCAAACAAAGCAAGTGTGGATAT 679

QY 202 CCTA 205

Db 680 CCAA 683

RESULT 44

AC118484/c

LOCUS

AC118484 165929 bp DNA linear HTG 18-JUL-2002

DEFINITION

Rattus norvegicus clone CH230-312N5, *** SEQUENCING IN PROGRESS
***, 46 unordered pieces.

ACCESSION

AC118484

KEYWORDS

HTG; HTGS_PHASE1.

SOURCE

Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 165929)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
 Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Chocko,J., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
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 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G. and Gibbs,R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 165929)
 Direct Submission
 Submitted (18-APR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

REFERENCE

AUTHORS

TITLE

JOURNAL

3 (bases 1 to 165929)
 Direct Submission
 Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Jul 14, 2002 this sequence version replaced gi:20177513.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GTTM

Center clone name: CH230-312N5

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 122701 bases at least Q40

Consensus quality: 128016 bases at least Q30

Consensus quality: 131913 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 46 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1280: contig of 1280 bp in length
 * 1281 1380: gap of unknown length
 * 1381 2480: contig of 1100 bp in length
 * 2481 2580: gap of unknown length
 * 2581 3861: contig of 1281 bp in length
 * 3862 3961: gap of unknown length
 * 3962 5807: contig of 1846 bp in length
 * 5808 5907: gap of unknown length
 * 5908 7452: contig of 1545 bp in length
 * 7453 7552: gap of unknown length
 * 7553 8983: contig of 1431 bp in length
 * 8984 9083: gap of unknown length
 * 9084 10115: contig of 1032 bp in length
 * 10116 10215: gap of unknown length
 * 10216 11728: contig of 1513 bp in length
 * 11729 11828: gap of unknown length
 * 11829 13698: contig of 1870 bp in length
 * 13699 13798: gap of unknown length
 * 13799 15150: contig of 1352 bp in length
 * 15151 15250: gap of unknown length
 * 15251 16756: contig of 1506 bp in length
 * 16757 16856: gap of unknown length
 * 16857 18576: contig of 1720 bp in length
 * 18577 18676: gap of unknown length
 * 18677 20170: contig of 1494 bp in length
 * 20171 20270: gap of unknown length
 * 20271 21819: contig of 1549 bp in length
 * 21820 21919: gap of unknown length
 * 21920 22925: contig of 1006 bp in length
 * 22926 23025: gap of unknown length
 * 23026 25396: contig of 2371 bp in length
 * 25397 25496: gap of unknown length
 * 25497 27382: contig of 1886 bp in length
 * 27383 27482: gap of unknown length
 * 27483 29578: contig of 2096 bp in length
 * 29579 29678: gap of unknown length
 * 29679 32138: contig of 2460 bp in length
 * 32139 32238: gap of unknown length
 * 32239 34391: contig of 2153 bp in length
 * 34392 34491: gap of unknown length
 * 34492 36897: contig of 2406 bp in length
 * 36898 36997: gap of unknown length
 * 36998 41252: contig of 4255 bp in length
 * 41253 41352: gap of unknown length
 * 41353 44626: contig of 3274 bp in length
 * 44627 44726: gap of unknown length
 * 44727 47515: contig of 2789 bp in length
 * 47516 47615: gap of unknown length
 * 47616 50485: contig of 2870 bp in length
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/rpt_type=DISPERSED
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/note="MER58B"
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/rpt_type=DISPERSED
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/rpt_type=DISPERSED
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/rpt_type=DISPERSED
complement(16187. .16488)

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Best Local Similarity 52.2%; Pred. No. 31;
Matches 71; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 66 CAAGAACAGGATAAAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAACT 125
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Db 243472 CAACAAAAGATAAACTCACTGAAGCTTCAGATAACCACTAGCATGTTTAGCAATAAAATT 243531
|||||
QY 126 TCCTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAAGGAGCCCATACCGAACAA 185
|||||
Db 243532 ATTTTAAACGAACATGCTACATTTTATAGAGATCATGCTATTATACACTTAATAGGCTAC 243591
|||||
QY 186 AGCAAGGTGTTATTAT 201
|||||
Db 243592 AGTATAGTAGATATAT 243607
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RESULT 46
AC092513
LOCUS AC092513 176350 bp DNA linear HTG 19-JUN-2002
DEFINITION Papio cynocephalus anubis clone RP41-474E21, WORKING DRAFT
SEQUENCE, 1 ordered piece.
AC092513
AC092513.2 GI:21465392
HTG; HTGS_PHASE2; HTGS_DRAFT.
olive baboon.
ORGANISM Papio cynocephalus anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
1 (bases 1 to 176350)
Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,
Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,
McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Schueler, M.G., Stanttripop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 176350)
Green, E.D.
Direct Submission
Submitted (13-JUL-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 176350)
Green, E.D.
Direct Submission
Submitted (19-JUN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jun 19, 2002 this sequence version replaced gi:14717326.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: aml
Center clone name: 474E21

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 176118 bases at least Q40
Consensus quality: 176233 bases at least Q30
Consensus quality: 176319 bases at least Q20
Insert size: 135000; agarose-fp
Insert size: 172000; pulse-field-gel
Insert size: 176350; sum-of-contigs
Quality coverage: 17.59x in Q20 bases; agarose-fp
Quality coverage: 13.81x in Q20 bases; pulse-field-gel
Quality coverage: 13.47x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 176350: contig of 176350 bp in length.
Location/Qualifiers
1. .176350

FEATURES
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clone end:T7
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AC092407 clone RP41-402M16 (center project name amk)"
136968. .176350
/note="clone overlaps with GenBank Accession Number
AC092515 clone RP41-66O1 (center project name ami)"
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Query Match 15.4%; Score 31.8; DB 2; Length 176350;
Best Local Similarity 54.8%; Pred. No. 34;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 23 ATACGAGTCTCTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAG 82
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Db 108096 ATTCAAATAGTTTATTCATTTGATAAAATAGCAATATTAGATACAGTAACAATATTAG 108155
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QY 83 AACTAAGCAACGGCGATACATAATTTGGTGGATGGCAACAACTTCCTGTGACTAA 137
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Db 108156 ATACTTTAAATGAAGGGTTTGGATGTTATTCACCACTTTAACTGAATAA 108210
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RESULT 47
AC094911
LOCUS
DEFINITION
Rattus norvegicus clone CH230-616, *** SEQUENCING IN PROGRESS ***,
70 unordered pieces.
AC094911
AC094911.3 GI:21716169
KEYWORDS
HTG; HTGS PHASE1.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 185829)

AUTHORS
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlssohn, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseghe, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,

Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.D., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Tang,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Thomas,S.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.

TITLE
JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Jul 9, 2002 this sequence version replaced gi:17941708.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GBRV
Center clone name: CH230-616
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 129832 bases at least Q40
Consensus quality: 134491 bases at least Q30
Consensus quality: 138158 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 70 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1095: contig of 1095 bp in length
* 1096 1195: gap of unknown length
* 1196 2369: contig of 1174 bp in length
* 2370 2469: gap of unknown length
* 2470 3565: contig of 1096 bp in length
* 3566 3665: gap of unknown length
* 3666 4898: contig of 1233 bp in length
* 4899 4998: gap of unknown length
* 4999 6162: contig of 1164 bp in length
* 6163 6262: gap of unknown length
* 6263 7595: contig of 1333 bp in length
* 7596 7695: gap of unknown length
* 7696 9145: contig of 1450 bp in length
* 9146 9245: gap of unknown length
* 9246 10909: contig of 1664 bp in length
* 10910 11009: gap of unknown length
* 11010 12428: contig of 1419 bp in length
* 12429 12528: gap of unknown length
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* 13575 13674: gap of unknown length
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* 15174 15273: gap of unknown length
* 15274 16614: contig of 1341 bp in length
* 16615 16714: gap of unknown length
* 16715 18176: contig of 1462 bp in length
* 18177 18276: gap of unknown length
* 18277 19907: contig of 1631 bp in length
* 19908 20007: gap of unknown length
* 20008 21342: contig of 1335 bp in length
* 21343 21442: gap of unknown length
* 21443 22868: contig of 1426 bp in length
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* 24393 26097: contig of 1705 bp in length
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* 27749 29614: contig of 1866 bp in length
* 29615 29714: gap of unknown length
* 29715 31099: contig of 1385 bp in length
* 31100 31199: gap of unknown length
* 31200 32224: contig of 1025 bp in length
* 32225 32324: gap of unknown length
* 32325 34335: contig of 2011 bp in length
* 34336 34435: gap of unknown length
* 34436 35741: contig of 1306 bp in length
* 35742 35841: gap of unknown length
* 35842 37125: contig of 1284 bp in length
* 37126 37225: gap of unknown length
* 37226 38820: contig of 1595 bp in length
* 38821 38920: gap of unknown length
* 38921 40969: contig of 2049 bp in length
* 40970 41069: gap of unknown length
* 41070 42637: contig of 1568 bp in length
* 42638 42737: gap of unknown length
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* 44249 44348: gap of unknown length
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* 46128 46227: gap of unknown length
* 46228 48028: contig of 1801 bp in length
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* 48129 51250: contig of 3122 bp in length
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* 53584 53683: gap of unknown length
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* 55685 55784: gap of unknown length
* 55785 58178: contig of 2394 bp in length
* 58179 58278: gap of unknown length
* 58279 61125: contig of 2847 bp in length
* 61126 61225: gap of unknown length
* 61226 62301: contig of 1076 bp in length
* 62302 62401: gap of unknown length
* 62402 64694: contig of 2293 bp in length
* 64695 64794: gap of unknown length
* 64795 66574: contig of 1780 bp in length
* 66575 66674: gap of unknown length
* 66675 68924: contig of 2250 bp in length
* 68925 69024: gap of unknown length
* 69025 71631: contig of 2607 bp in length
* 71632 71731: gap of unknown length
* 71732 74590: contig of 2859 bp in length
* 74591 74690: gap of unknown length
* 74691 77085: contig of 2395 bp in length
* 77086 77185: gap of unknown length
* 77186 79602: contig of 2417 bp in length
* 79603 79702: gap of unknown length
* 79703 83597: contig of 3895 bp in length
* 83598 83697: gap of unknown length
* 83698 86247: contig of 2550' bp in length
* 86248 86347: gap of unknown length

ORIGIN

Query Match 15.3%; Score 31.6; DB 9; Length 157750;
Best Local Similarity 52.2%; Pred. No. 40;
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 34 TGGTCAATTCAGGACACAGATGATCGGTCCAGAACAGAGATAATAGAACTAAGCAAC 93
|||||
Db 104456 TGGTCAATTTGATTTTTTTCACATGTTGGTTAAAGACAGAGGTGCCAGATAAAATACAG 104515
|||||
QY 94 GCGATACAAATTTGGTGGATTGGCAACAACAACTTCCTGTGACTAAACAGGTCCATAGTTT 153
|
Db 104516 GATGACCAAGTTAAGTTGAATATGGGACATACATCTTATATTAAAAAATTATTTATTGTT 104575
|
QY 154 CACGACACTTCCAA 167
|
Db 104576 TATGTAACCTCCAAA 104589
|

RESULT 51

AC108799 205615 bp DNA linear HTG 25-APR-2002
LOCUS Mus musculus clone RP23-119G12, WORKING DRAFT SEQUENCE, 23 ordered
DEFINITION pieces.
ACCESSION AC108799
VERSION AC108799.2 GI:20303809
KEYWORDS HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus.
ORGANISM Mus musculus

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL 1 (bases 1 to 205615)
REFERENCE Birren, B., Linton, L., Nusbaum, C. and Lander, E.
AUTHORS Mus musculus, clone RP23-119G12
2 (bases 1 to 205615)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL Direct Submission
Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

AUTHORS 3 (bases 1 to 205615)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepe, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL Direct Submission
Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 25, 2002 this sequence version replaced gi:18450059.

COMMENT

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L20730

Center clone name: 119 G 12

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 198517 bases at least Q40

Consensus quality: 201511 bases at least Q30

Consensus quality: 202745 bases at least Q20

Insert size: 207000; agarose-fp

Insert size: 203415; sum-of-contigs

Quality coverage: 5.3 in Q20 bases; agarose-fp

Quality coverage: 5.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 23 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 85: contig of 85 bp in length

* 86 185: gap of 100 bp

* 186 32349: contig of 32164 bp in length

* 32350 32449: gap of 100 bp

* 32450 33486: contig of 1037 bp in length

* 33487 33586: gap of 100 bp

* 33587 35126: contig of 1540 bp in length

* 35127 35226: gap of 100 bp

* 35227 36323: contig of 1097 bp in length

* 36324 36423: gap of 100 bp

* 36424 37345: contig of 922 bp in length

* 37346 37445: gap of 100 bp

* 37446 40096: contig of 2651 bp in length

* 40097 40196: gap of 100 bp

* 40197 42396: contig of 2200 bp in length

* 42397 42496: gap of 100 bp

* 42497 44779: contig of 2283 bp in length

* 44780 44879: gap of 100 bp

* 44880 46918: contig of 2039 bp in length

* 46919 47018: gap of 100 bp

* 47019 50053: contig of 3035 bp in length

* 50054 50153: gap of 100 bp

* 50154 55789: contig of 5636 bp in length

* 55790 55889: gap of 100 bp

* 55890 61419: contig of 5530 bp in length

* 61420 61519: gap of 100 bp

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Dδ	1884 AACAGCTCCAAAGCCACCAATATCAGCTCCAAGGGCGGCATACCCCATCAAATCAAAAATGC	1943 				
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Dδ	1944 TACTA	1948 				

RESULT	53
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DEFINITION	S.cerevisiae CLA4 gene.
ACCESSION	X82499
VERSION	X82499.1 GI:732943
KEYWORDS	CLA4 gene; protein kinase.
SOURCE	Saccharomyces cerevisiae.
ORGANISM	Saccharomyces cerevisiae Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. 1 (bases 1 to 3858) Cvrckova,F. Direct Submission Submitted (03-NOV-1994) F. Cvrckova, IMP, Dr Bohr-Gasse 7, 1030 Wien, AUSTRIA 2 (bases 1 to 3858) Cvrckova,F., De Virgilio,C., Manser,E., Pringle,J.R. and Nasmyth,K. Ste20-like protein kinases are required for normal localization of cell growth and for cytokinesis in budding yeast Genes Dev. 9 (15), 1817-1830 (1995)
JOURNAL	95377634
MEDLINE	7649470
PUBMED	

FEATURES

source

Location/Qualifiers

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BASE COUNT

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Query Match 15.2%; Score 31.4; DB 8; Length 3858;

[illegible]

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DEFINITION	Saccharomyces cerevisiae chromosome XIV, 30 Kb fragment.						
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VERSION	U23084.1 GI:1050853						
KEYWORDS	.						
SOURCE	Saccharomyces cerevisiae.						
ORGANISM	Saccharomyces cerevisiae						
	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;						
	Saccharomycetales; Saccharomycetaceae; Saccharomyces.						
REFERENCE	1 (bases 1 to 30003)						
AUTHORS	Maurer, K.C., Urbanus, J.H. and Planta, R.J.						
TITLE	Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, and a novel putative serine/threonine protein kinase gene						
JOURNAL	Yeast 11 (13), 1303-1310 (1995)						
MEDLINE	96132033						
PUBMED	8553702						
REFERENCE	2 (bases 1 to 30003)						
AUTHORS	Maurer, K.T.C.						
TITLE	Direct Submission						
JOURNAL	Submitted (21-MAR-1995) Kick T.C. Maurer, Biochemistry and						

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Best Local Similarity 67.7%; Pred. No. 43;
Matches 44; Conservative 0; Mismatches 21; Indels 0; Gaps 0;


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Db 12755 AACAGTCCAAAGCCACCAATATCAGCTCCAAAGGCGCCATACCCATCAAAATGC 12814

Qy 196 TATTA 200
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Db 12815 TACTA 12819

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DEFINITION AC102032
ACCESSION AC102032
VERSION AC102032.1 GI:17061118
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus
ORGANISM Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 64656)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-78J18
Unpublished
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
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Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
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Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
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Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L17941
Center clone name: 78_J_18
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* NOTE: This record contains 81 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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* 43852 44570: contig of 719 bp in length
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* 44671 45355: contig of 685 bp in length
* 45356 45455: gap of 100 bp
* 45456 46166: contig of 711 bp in length
* 46167 46266: gap of 100 bp
* 46267 46977: contig of 711 bp in length
* 46978 47077: gap of 100 bp
* 47078 47781: contig of 704 bp in length
* 47782 47881: gap of 100 bp
* 47882 48601: contig of 720 bp in length
* 48602 48701: gap of 100 bp
* 48702 49398: contig of 697 bp in length
* 49399 49498: gap of 100 bp
* 49499 50183: contig of 685 bp in length
* 50184 50283: gap of 100 bp
* 50284 50992: contig of 709 bp in length
* 50993 51092: gap of 100 bp
* 51093 51775: contig of 683 bp in length
* 51776 51875: gap of 100 bp
* 51876 52583: contig of 708 bp in length
* 52584 52683: gap of 100 bp
* 52684 53394: contig of 711 bp in length
* 53395 53494: gap of 100 bp
* 53495 54206: contig of 712 bp in length
* 54207 54306: gap of 100 bp
* 54307 55024: contig of 718 bp in length
* 55025 55124: gap of 100 bp

Query Match 15.2%; Score 31.4; DB 2; Length 64656;
Best Local Similarity 56.2%; Pred. No. 44;
Matches 59; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 35 GGTCATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACG 94
|||||
Db 8830 GGTCCTTTAAGAAGGACATACATAACTCCCTTACAGAAACAGGAAATACAGGTAACAAAGT 8889
|||||

QY 95 CGATACAAATTGGTGGATTGGCAACAACTTCTGTGACTAACA 139
|||
Db 8890 AGAAGCCCTTAAAGTGGAAACACAAAATCCCTTAAAGAAATCACA 8934
|||
RESULT 56
AL138731 72312 bp DNA linear PRI 22-MAR-2001
LOCUS Human DNA sequence from clone RP1-23E21 on chromosome 6 Contains a
DEFINITION pseudogene similar to JAB1, an STS and GSSs, complete sequence.
ACCESSION AL138731
VERSION AL138731.10 GI:11120990
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 72312)
AUTHORS Corby,N.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

COMMENT
On Nov 8, 2000 this sequence version replaced gi:10880142.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C/elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6

IMPORTANT: This sequence is not the entire insert of clone
RP1-23E21 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-346N8 is at 72213 in this sequence.
The true right end of clone RP11-538A16 is at 100 in this sequence.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RP1-23E21 is from the
library RPCI-1 constructed by the group of Pieter de Jong. For
further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.

FEATURES
source
1. .72312
/location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP1-23E21"
/clone_lib="RPCI-1"
repeat_region 1. .81
/note="MSTA repeat: matches 4. .84 of consensus"
repeat_region 94. .190
/note="MIR repeat: matches 49. .151 of consensus"
repeat_region 297. .616
/note="160 copies 2 mer aa 59% conserved"
repeat_region 340. .615
/note="12 copies 23 mer 64% conserved"
repeat_region 1347. .1598
/note="Tigger3b repeat: matches 979. .1241 of consensus"

repeat_region 1579. .2412
/note="Tigger3b repeat: matches 1. .849 of consensus"
repeat_region 3193. .3335
/note="MLT1I repeat: matches 230. .354 of consensus"
repeat_region 5862. .5939
/note="L2 repeat: matches 2628. .2710 of consensus"
repeat_region 8707. .8817
/note="MIR repeat: matches 100. .204 of consensus"
repeat_region 9528. .9587
/note="15 copies 4 mer tgtg 98% conserved"
repeat_region 10027. .10219
/note="LTR16A repeat: matches 217. .436 of consensus"
repeat_region 11084. .11366
/note="AluY repeat: matches 12. .293 of consensus"
repeat_region 11403. .11511
/note="AluSc repeat: matches 244. .299 of consensus"
repeat_region 11584. .11830
/note="AluY repeat: matches 1. .249 of consensus"
repeat_region 12009. .12075
/note="MLT1J repeat: matches 304. .367 of consensus"
repeat_region 14318. .14525
/note="MIR repeat: matches 46. .257 of consensus"
repeat_region 15291. .15512
/note="111 copies 2 mer aa 56% conserved"
repeat_region 15631. .16691
/note="MER11C repeat: matches 1. .1071 of consensus"
repeat_region 17046. .17494
/note="L1M4 repeat: matches 3108. .3556 of consensus"
misc_feature complement(17483. .18190)
/note="match: GSS: Em:AQ528649"
misc_feature complement(17517. .18188)
/note="match: GSS: Em:AQ528680"
repeat_region 17620. .17647
/note="14 copies 2 mer ac 92% conserved"
misc_feature complement(17689. .18181)
/note="match: GSS: Em:AQ182012"
misc_feature complement(17919. .18184)
/note="match: GSS: Em:AQ774948"
repeat_region 18089. .18447
/note="MER34 repeat: matches 211. .545 of consensus"
repeat_region 18496. .18722
/note="MER30 repeat: matches 1. .230 of consensus"
repeat_region 18750. .18924
/note="MER34 repeat: matches 8. .175 of consensus"
misc_feature 18786. .19128
/note="match: GSS: Em:B41655"
repeat_region 19757. .19889
/note="MIR repeat: matches 54. .190 of consensus"
repeat_region 20856. .20994
/note="MIR repeat: matches 29. .175 of consensus"
repeat_region 21044. .21135
/note="4 copies 23 mer 90% conserved"
repeat_region 23383. .23734
/note="MLT1A2 repeat: matches 7. .369 of consensus"
repeat_region 27384. .27554
/note="MIR repeat: matches 87. .261 of consensus"
repeat_region 28170. .28330
/note="AluSg/x repeat: matches 135. .295 of consensus"
repeat_region 30448. .30471
/note="MIR repeat: matches 183. .205 of consensus"
repeat_region 30472. .30509
/note="L2 repeat: matches 2648. .2685 of consensus"
repeat_region 30510. .30524
/note="MIR repeat: matches 205. .261 of consensus"
misc_feature complement(32107. .33024)
/note="match: GSS: Em:AQ743106"
misc_feature complement(32486. .33025)
/note="match: GSS: Em:AQ542518"
repeat_region 32593. .32717
/note="FLAM C repeat: matches 1. .125 of consensus"
misc_feature 33019. .33473
/note="match: GSS: Em:AQ593411"
misc_feature complement(33062. .33656)

misc_feature /note="match: GSS: Em:AQ419443"
33104. .33519
/note="match: GSS: Em:AQ090303"
33130. .33249
/note="60 copies 2 mer aa 61% conserved"
misc_feature complement(33264. .33659)
/note="match: GSS: Em:AQ090546"
33775. .33800
/note="13 copies 2 mer ag 92% conserved"
34206. .34800
/note="match: GSS: Em:AQ035350"
gene complement(34676. .35581)
/gene="dJ23E21.1"
CDS complement(34676. .35581)
/gene="dJ23E21.1"
/note="dJ23E21.1 (similar to JAB1)
match: proteins: Tr:O15386 Tr:O35864"
/pseudo
/codon_start=1
/evidence=not_experimental
repeat_region 35714. .36025
/note="AluSx repeat: matches 1. .312 of consensus"
repeat_region 37734. .37761
/note="14 copies 2 mer ac 100% conserved"
repeat_region 38271. .38566
/note="AluSc repeat: matches 1. .301 of consensus"
repeat_region 40486. .40785
/note="MER33 repeat: matches 1. .324 of consensus"
repeat_region 41311. .41391
/note="MADE1 repeat: matches 1. .80 of consensus"
repeat_region 41784. .42179
/note="LiMEC repeat: matches 1337. .1698 of consensus"
misc_feature complement(42277. .43029)
/note="match: GSS: Em:AQ742617"
repeat_region 43111. .43162
/note="L2 repeat: matches 2699. .2750 of consensus"
repeat_region 43163. .43459
/note="AluSx repeat: matches 1. .297 of consensus"
repeat_region 43460. .43470
/note="L2 repeat: matches 2648. .2700 of consensus"
repeat_region 43605. .44064
/note="L2 repeat: matches 1997. .2445 of consensus"
repeat_region 44142. .44368
/note="MLT1A1 repeat: matches 138. .365 of consensus"
repeat_region 44373. .44570
/note="L2 repeat: matches 1747. .1966 of consensus"
repeat_region 44669. .44823
/note="FRAM repeat: matches 0. .152 of consensus"
repeat_region 45847. .46142
/note="AluY repeat: matches 1. .296 of consensus"
misc_feature complement(46105. .46452)
/note="match: GSS: Em:AQ817722"
repeat_region 46261. .46313
/note="MADE1 repeat: matches 28. .80 of consensus"
misc_feature 46561. .47041
/note="match: STS: Em:G61943
match: GSS: Em:AQ285562"
repeat_region 49795. .49939
/note="L2 repeat: matches 1155. .1293 of consensus"
repeat_region 49940. .50251
/note="AluJo repeat: matches 1. .296 of consensus"
repeat_region 50252. .50968

Query Match 15.2%; Score 31.4; DB 9; Length 72312;
Best Local Similarity 57.7%; Pred.No. 45;
Matches 56; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 27 GAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAAATACT 86
Db 42190 GAGTTGGGGGCAAGAACTAGCAGACGCTCATTTGCTAGAGAGAGAAAAAATACT 42249
QY 87 AAGCAACGGGATACAAATTTGGTGGATTGGCAACAAA 123

Db 42250 TGGCAAAATTGTGAAGCTGGATGAAATTAGGCATCAA 42286

RESULT 57
AC091647

LOCUS AC091647 173368 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens chromosome 18, clone RP11-635D8, complete sequence.
AC091647
VERSION AC091647.4 GI:18093025
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 173368)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 18, clone RP11-635D8
Unpublished

2 (bases 1 to 173368)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K.,
Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
Iliev,I., Johnson,R., Jones,C., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (13-MAY-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 173368)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (09-AUG-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 173368)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,

Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (09-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jan 9, 2002 this sequence version replaced gi:15145252.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L13183

Center clone name: 635_D_8

SP6 end overlaps AC011155 [WICGR project L2947; in finishing] by
48307 bp;

T7 end overlaps AC019239 [WICGR project L1005] by 143942 bp. We
will submit the

entire L13183 clone [29426 bp unique unsubmitted a/o 8/4/01
sequence].

FEATURES	Location/Qualifiers
source	1. 173368 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="18" /map="18"
unsure	/clone="RP11-635D8" 4. .43 /clone_lib="RPC1-11 Human Male BAC"
unsure	/note="<30 qual SNGL region"
unsure	48. 105 /note="<30 qual SNGL region"
unsure	136. 140 /note="<30 qual SNGL region"
unsure	171. 175 /note="<30 qual SNGL region"
unsure	204. 214 /note="<30 qual SNGL region"
unsure	247. 253 /note="<30 qual SNGL region"
repeat_region	817. 1019 /rpt_family="MIR"
repeat_region	1365. 1450 /rpt_family="(TATATG)n"
repeat_region	1643. 1695 /rpt_family="(CATATA)n"
unsure	1912. 1916 /note="<30 qual SNGL region"
unsure	2114. 2118 /note="<30 qual SNGL region"
repeat_region	2604. 2648


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/rpt_family="(TCTA)n"
2778. .2802
/rpt_family="AT_rich"
2920. .2932
/note="<30 qual SNGL region"
complement(3266. .3550)
/rpt_family="AluSg"
complement(4643. .4797)
/rpt_family="L2"
complement(4904. .7127)
/rpt_family="L1p"
complement(8029. .8334)
/rpt_family="AluSg"
complement(9055. .9208)
/rpt_family="MIR"
9589. .9740
/rpt_family="MER5A"
complement(13365. .13568)
/rpt_family="MIR"
complement(14097. .14266)
/rpt_family="L1MA4A"
14917. .15064
/rpt_family="MIR"
complement(16054. .16296)
/rpt_family="MIR"
complement(16317. .16458)
/rpt_family="MIR3"
16563. .16623
/rpt_family="GA-rich"
16980. .17093
/rpt_family="(TTCC)n"
17906. .17936
/rpt_family="AT_rich"
complement(18341. .18541)
/rpt_family="MIR"
complement(19374. .19719)
/rpt_family="L2"
20270. .20457
/rpt_family="MER5A"
complement(20621. .20696)
/rpt_family="L2"
20720. .20753
/rpt_family="polypurine"
21715. .21750
/rpt_family="AT_rich"
complement(22572. .22616)
/rpt_family="MIR"
23433. .23606
/rpt_family="MER20"
23819. .23846
/rpt_family="AT_rich"
24483. .24510
/rpt_family="(TG)n"
complement(25633. .25703)
/rpt_family="MER5A"
25648. .25779
/rpt_family="MER5A"
complement(25798. .25822)
/rpt_family="MIR"
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Query Match      15.2%; Score 31.4; DB 9; Length 173368;
Best Local Similarity 64.4%; Pred. No. 46;
Matches 47; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 32 CTTGGTCAATTTCAGGACACAGATGATTCGGTCCAAAGACAGGATAATAGAACTAAGCA 91
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 900 CTTAGGCAATTTCTGGGCACAAATGTCTGTCTGCCAAACGGAGATAAGATCCTACCT 959
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 92 ACGGATACAATT 104
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 960 ACCTGATACAAT 972
```

```
RESULT 58
AP001484
LOCUS
DEFINITION
Homo sapiens chromosome 18 clone RP11-635D8 map 18q21, WORKING
DRAFT SEQUENCE, 41 unordered pieces.
ACCESSION
AP001484.2 GI:8117342
VERSION
HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
Homo sapiens DNA, clone:RP11-635D8.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 185479)
AUTHORS
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 185,479 genomic DNA of 18q21
Published Only in DataBase (2000)
TITLE
2 (bases 1 to 185479)
JOURNAL
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
REFERENCE
Direct Submission
AUTHORS
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE
Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
COMMENT
On May 30, 2000 this sequence version replaced gi:7288178.
```

```
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft18
Center clone name: RP11-635D8
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 167208 bases at least Q40
Consensus quality: 172243 bases at least Q30
Consensus quality: 176665 bases at least Q20
Insert size: 181479; sum-of-contigs
Quality coverage: 5.04x in Q20 bases; sum-of-contigs
```

NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1	16288	contig of	16288	bp in length
16389	25442	contig of	9054	bp in length
25543	35229	contig of	9687	bp in length
35330	43767	contig of	8438	bp in length
43868	52274	contig of	8407	bp in length
52375	60076	contig of	7702	bp in length
60177	67220	contig of	7044	bp in length
67321	73733	contig of	6413	bp in length
73834	79587	contig of	5754	bp in length
79688	86110	contig of	6423	bp in length
86211	91829	contig of	5619	bp in length
91930	98330	contig of	6401	bp in length
98431	102918	contig of	4488	bp in length
103019	107979	contig of	4961	bp in length
108080	113581	contig of	5502	bp in length
113682	117572	contig of	3891	bp in length
117673	122375	contig of	4703	bp in length
122476	127400	contig of	4925	bp in length
127501	130555	contig of	3055	bp in length
130656	134486	contig of	3831	bp in length

DEFINITION

Mus musculus clone RP23-401D18, WORKING DRAFT SEQUENCE, 13 unordered pieces.

ACCESSION

AC099591

VERSION

AC099591.1 GI:16946040

KEYWORDS

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE

Mus musculus.

ORGANISM.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 190519)

AUTHORS

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

JOURNAL

Mus musculus, clone RP23-401D18

REFERENCE

2 (bases 1 to 190519)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

Direct Submission

JOURNAL

Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L17159

Center clone name: 401.D18

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 187719 bases at least Q40

Consensus quality: 188683 bases at least Q30

Consensus quality: 188965 bases at least Q20

Insert size: 190000; agarose-fp

Insert size: 189319; sum-of-contigs

Quality coverage: 13.0 in Q20 bases; agarose-fp

Quality coverage: 13.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 2300: contig of 2300 bp in length

* 2301 2400: gap of 100 bp

* 2401 3604: contig of 1204 bp in length

* 3605 3704: gap of 100 bp
* 3705 4712: contig of 1008 bp in length
* 4713 4812: gap of 100 bp
* 4813 6035: contig of 1223 bp in length
* 6036 6135: gap of 100 bp
* 6136 7649: contig of 1514 bp in length
* 7650 7749: gap of 100 bp
* 7750 11022: contig of 3273 bp in length
* 11023 11122: gap of 100 bp
* 11123 85122: contig of 74000 bp in length
* 85123 85222: gap of 100 bp
* 85223 92356: contig of 7134 bp in length
* 92357 92456: gap of 100 bp
* 92457 105968: contig of 13512 bp in length
* 105969 106068: gap of 100 bp
* 106069 128004: contig of 21936 bp in length
* 128005 128104: gap of 100 bp
* 128105 152627: contig of 24523 bp in length
* 152628 152727: gap of 100 bp
* 152728 187127: contig of 34400 bp in length
* 187128 187227: gap of 100 bp
* 187228 190519: contig of 3292 bp in length.

FEATURES

source

1..190519
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-401D18"
/clone_lib="RPCI-23 Female Mouse BAC"

misc_feature

1..2300
/note="assembly_fragment"
clone_end:SP6
vector_side:left

misc_feature

2401..3604
/note="assembly_fragment"

misc_feature

3705..4712
/note="assembly_fragment"

misc_feature

4813..6035
/note="assembly_fragment"

misc_feature

6136..7649
/note="assembly_fragment"

misc_feature

7750..11022
/note="assembly_fragment"

misc_feature

11123..85122
/note="assembly_fragment"

misc_feature

85223..92356
/note="assembly_fragment"

misc_feature

92457..105968
/note="assembly_fragment"

misc_feature

106069..128004
/note="assembly_fragment"

misc_feature

128105..152627
/note="assembly_fragment"

misc_feature

152728..187127
/note="assembly_fragment"

misc_feature

187228..190519
/note="assembly_fragment"

misc_feature

clone_end:T7
vector_side:right

misc_feature

BASE COUNT 59067 a 35291 c 35289 g 59637 t 1235 others

ORIGIN

Query Match 15.2%; Score 31.4; DB 2; Length 190519;
Best Local Similarity 53.7%; Pred. No. 46;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 33 TTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATATAGAACTAAGCAA 92

Db 51882 TAGATAAAATATCCAAACATATGATTCACATATAAAGAAAGGAAA 51941

QY 93 CGGATACAATTTGGTGGATTGGCAACAACCTCTCTGTGACTAACAGGTCCATAGTTT 152

Db 51942 AAAGAAATATTTTCCATCATTTTGTAGAAAATTTACTGTCTATTAGAAAATGTAAGTTT 52001

```
QY 153 T 153
Db 52002 T 52002

RESULT 60
AL844585/c
LOCUS
DEFINITION Mus musculus chromosome 4 clone RP23-339I5, *** SEQUENCING IN
PROGRESS ***, 5 unordered pieces.
AL844585
AL844585.5 GI:22416220
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 200512)
Andrew, R.
Direct Submission
Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 21, 2002 this sequence version replaced gi:2265574.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM339I5
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 199640 bases at least Q40
Consensus quality: 199960 bases at least Q30
Consensus quality: 200067 bases at least Q20
Insert size: 200112; sum-of-contigs
Insert size: 191990; 6.6% error; agarose-fp
Quality coverage: 11.28x in Q20 bases; sum-of-contigs Quality
coverage: 11.97x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 68877: contig of 68877 bp in length
* 68878 68977: gap of 100 bp
* 68978 83970: contig of 14993 bp in length
* 83971 84070: gap of 100 bp
* 84071 101123: contig of 17053 bp in length
* 101124 101223: gap of 100 bp
* 101224 198044: contig of 96821 bp in length
* 198045 198144: gap of 100 bp
* 198145 200512: contig of 2368 bp in length.
FEATURES
source
1..200512
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-339I5"
/clone_lib="RPCI-23"
/misc_feature 1..68877
/note="assembly_fragment:02211
fragment_chain:1"
68978..83970
/misc_feature
/note="assembly_fragment:00776
fragment_chain:1"
84071..101123
misc_feature
/note="assembly_fragment:04201
fragment_chain:1"
101224..198044
/misc_feature
/note="assembly_fragment:00213"
198145..200512
/note="assembly_fragment:03592"

BASE COUNT 55849 a 41861 c 43308 g 59094 t 400 others
ORIGIN

Query Match 15.2%; Score 31.4; DB 2; Length 200512;
Best Local Similarity 51.0%; Pred. No. 47;
Matches 74; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 61 CGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAAC 120
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 32847 CGAGCAAAGAACAGAAATAATTAATTAAACAATGTCAGAAATATTCGATTTTGTAAATATC 32788

QY 121 AAATTCTGTGACTAAACAGGTCCATAGTTTTCACGACACTTCCAGGACGCCATACCG 180
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 32787 CTTGTCCAACAATAACAAAATCTTTATATCTAGGTAAATCCCAAGTATTACATATAT 32728

QY 181 AACAAAGCAAGGTGTTATTATCCTA 205
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 32727 AACAGAGACATGTTAAATAATAATA 32703

RESULT 61
AF208338
LOCUS
DEFINITION Streptocarpus holstii Gcyc1A protein (Gcyc1A) gene, partial cds.
ACCESSION AF208338
VERSION AF208338.1 GI:8650371
KEYWORDS
SOURCE Streptocarpus holstii.
ORGANISM Streptocarpus holstii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Gesneriaceae; Streptocarpus.
1 (bases 1 to 591)
Citerne, H., Moeller, M. and Cronk, Q.C.B.
Diversity of cycloidea-like genes in Gesneriaceae in relation to
floral symmetry
Ann. Bot. 86 (1), 167-176 (2000)
2 (bases 1 to 591)
Citerne, H.
Direct Submission
Submitted (19-NOV-1999) Royal Botanic Garden Edinburgh, 20A
Inverleith Row, Edinburgh EH3 5LR, UK
FEATURES
Location/Qualifiers
source
1..591
/organism="Streptocarpus holstii"
/db_xref="taxon:28536"
<1..>591
/gene="Gcyc1A"
<1..>591
/gene="Gcyc1A"
/product="Gcyc1A protein"
<1..591
/gene="Gcyc1A"
/codon_start=1
/product="Gcyc1A protein"
/protein_id="AAF78181.1"
/db_xref="GI:8650372"
/translation="MLGFDKPSKTLDWLLTKSKVAIKDLVLTNKSSSSRSPSPSECE
VALNDEAFQDGSCLLPDSKRNASTARDPAQSASTLAKESRAKARARERTKEKLC
IKKLNESRNMNNLFTSNQPVLHCPITNEATATQDLIQESSVIKRMRLRHQSFPGF
HCAALPSPDVNENWDAGSLTSQSNLCLDQHKFIN"

BASE COUNT 186 a 140 c 125 g 137 t 3 others
ORIGIN

Query Match 15.1%; Score 31.2; DB 8; Length 591;
Best Local Similarity 49.3%; Pred. No. 42;
Matches 75; Conservative 2; Mismatches 75; Indels 0; Gaps 0;
```


This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org> VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-219G10, 2000 bp overlap; the clone sequenced to the right is RP11-756P10, 2000 bp overlap. Actual start of this clone is at base position 155040 of RP11-219G10; actual end is at base position 72504 of RP11-756P10.

Polymorphisms have been identified between AC011729, AC022189, and AC114759. Data from AC011729 and AC022189 was used to finish this clone, AC114759.

FEATURES

source

Location/Qualifiers

1. 80436
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-347K3"
/clone_lib="RPCI-11"

6. 98
/rpt_family="L1"
99. 408
/rpt_family="Alu"
409. 742
/rpt_family="L1"
954. 1090
/rpt_family="MER2_type"
1092. 1158
/rpt_family="MER2_type"
1159. 1366
/rpt_family="MER1_type"
1367. 1563
/rpt_family="MER2_type"
1564. 1697
/rpt_family="L1"
1790. 1938
/rpt_family="L1"
2889. 3013
/rpt_family="L2"
4725. 5028
/rpt_family="Alu"
5683. 5884
/rpt_family="L2"
6679. 6839
/rpt_family="L2"
9410. 9696
/rpt_family="Alu"
9947. 9999
/rpt_family="MIR"
11556. 11710
/rpt_family="MIR"

repeat_region 11909. 11947
/rpt_family="(GA)n"
repeat_region 11961. 12097
/rpt_family="L2"
repeat_region 12713. 13152
/rpt_family="L2"
repeat_region 13298. 13462
/rpt_family="AcHobo"
13466. 13849
/rpt_family="AcHobo"
repeat_region 13850. 14147
/rpt_family="Alu"
repeat_region 14148. 14480
/rpt_family="AcHobo"
repeat_region 14483. 14899
/rpt_family="L1"
repeat_region 14962. 15120
/rpt_family="Alu"
repeat_region 15121. 15211
/rpt_family="(TA)n"
repeat_region 15394. 15583
/rpt_family="MER2_type"
repeat_region 15593. 15698
/rpt_family="Alu"
repeat_region 15731. 15898
/rpt_family="MER2_type"
repeat_region 21930. 22005
/rpt_family="MER2_type"
repeat_region 22006. 22083
/rpt_family="(TATG)n"
repeat_region 22225. 22249
/rpt_family="AT_rich"
repeat_region 22306. 22333
/rpt_family="AT_rich"
repeat_region 23279. 23668
/rpt_family="L1"
repeat_region 23669. 23952
/rpt_family="Alu"
repeat_region 23953. 25633
/rpt_family="L1"
repeat_region 25634. 25675
/rpt_family="(TTTA)n"
repeat_region 25676. 25841
/rpt_family="L1"
repeat_region 25844. 26090
/rpt_family="L1"
repeat_region 26097. 26187
/rpt_family="L1"
repeat_region 26203. 26520
/rpt_family="L1"
repeat_region 27010. 27229
/rpt_family="MIR"
repeat_region 27433. 27456
/rpt_family="AT_rich"
repeat_region 28035. 28192
/rpt_family="L1"
repeat_region 28718. 28920
/rpt_family="ERV1"
repeat_region 28944. 29837
/rpt_family="L1"
repeat_region 31177. 31538
/rpt_family="MaLR"
repeat_region 31929. 32490
/rpt_family="MaLR"
repeat_region 32845. 33173
/rpt_family="ERV1"
repeat_region 33193. 33277
/rpt_family="CR1"
repeat_region 34606. 34920
/rpt_family="Alu"

Query Match 15.1%; Score 31.2; DB 9; Length 80436;
Best Local Similarity 47.9%; Pred. No. 52;

REFERENCE

6 (bases 1 to 142992)
Waterston,R.
Direct Submission

Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE

7 (bases 1 to 142992)
Waterston,R.
Direct Submission
Submitted (21-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jul 17, 1999 this sequence version replaced gi:3213159.

COMMENT

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

Center project name: H_DJ0589D08

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/OTB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at <http://www.chori.org> using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc.

(<http://www.genomesystems.com>) or Research Genetics, Inc.

(<http://www.resgen.com>); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is DJ1166A24, 200 bp overlap.

Actual start of this clone is at base position 1 of DJ0589D08;

actual end is at 15237 of DJ1166A24.

FEATURES

source

Location/Qualifiers

1. 142992

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="7"

/map="7q31.1-q31.3"

/clone="RP4-589D8"

/clone_lib="RPCI-4"

676..763

/rpt_family="CT-rich"

1079..1383

/rpt_family="Alu"

1551..1727

/rpt_family="MER1_type"

2256..2339

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region
3456..4102
/rpt_family="L1"
4122..4248
/rpt_family="MER1_type"
4477..4559
/rpt_family="MaLR"
4558..4666
/rpt_family="MaLR"
5135..5194
/rpt_family="L2"
5330..5435
/rpt_family=" (TA)n"
6042..6110
/rpt_family="AT-rich"
6215..6341
/rpt_family="L1"
7129..7152
/rpt_family="AT-rich"
7530..7745
/rpt_family="MaLR"
7861..8312
/rpt_family="L1"
8404..8472
/rpt_family=" (TA)n"
8501..8591
/rpt_family=" (TA)n"
12297..12359
/rpt_family=" (TC)n"
14331..14644
/rpt_family="Alu"
14843..14876
/rpt_family=" (CA)n"
15301..15335
/rpt_family="SS"
15336..15623
/rpt_family="Alu"
15626..15773
/rpt_family="GA-rich"
18791..19205
/rpt_family="Retroviral"
19259..19815
/rpt_family="L1"
19837..19909
/rpt_family=" (TA)n"
19975..20862
/rpt_family="L1"
20993..21063
/rpt_family=" (TA)n"
21069..21148
/rpt_family="L1"
21156..21178
/rpt_family="AT-rich"
21211..21368
/rpt_family="L1"
21357..21593
/rpt_family="L1"
22521..22661
/rpt_family="MER1_type"
22544..22665
/rpt_family="MER1_type"
23567..23778
/rpt_family="MER1_type"
24334..24365
/rpt_family="AT-rich"
24366..24399
/rpt_family=" (TCTA)n"
25598..25612
/rpt_family="AT-rich"
25613..25895
/rpt_family="Alu"
25896..25945
/rpt_family="AT-rich"

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 6179: contig of 6179 bp in length
6180 6279: gap of 100 bp
6280 13404: contig of 7125 bp in length
13405 13504: gap of 100 bp
13505 21030: contig of 7526 bp in length
21031 21130: gap of 100 bp
21131 30422: contig of 9292 bp in length
30423 30522: gap of 100 bp
30523 50525: contig of 20003 bp in length
50526 50625: gap of 100 bp
50626 69401: contig of 18776 bp in length
69402 69501: gap of 100 bp
69502 100507: contig of 31006 bp in length
100508 100607: gap of 100 bp
100608 146118: contig of 45511 bp in length.

FEATURES

source
1. 146118
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-16L12"
/clone_lib="RP11-16L12"
/clone_lib="RP11-16L12"
1. 6179
/note="assembly_fragment"
6280. 13404
/note="assembly_fragment"
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Query Match 15.1%; Score 31.2; DB 2; Length 146118;
Best Local Similarity 47.9%; Pred. No. 53;
Matches 90; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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LOCUS Homo sapiens chromosome 11 clone RP11-16M7 map 11, WORKING DRAFT
DEFINITION SEQUENCE, 16 unordered pieces.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

AC022189
AC022189.2 GI:7230131
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-16M7
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepell,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
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Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
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Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (26-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2000 this sequence version replaced gi:6759180.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3585
Center clone name: 16 M 7
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 136081 bases at least Q40
Consensus quality: 141411 bases at least Q30
Consensus quality: 143388 bases at least Q20
Insert size: 148000; agarose-fp
Insert size: 145025; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1603: contig of 1603 bp in length
1604 1703: gap of 100 bp
1704 3721: contig of 2018 bp in length
3722 3821: gap of 100 bp
3822 6237: contig of 2416 bp in length
6238 6337: gap of 100 bp
6338 8767: contig of 2430 bp in length
8768 8867: gap of 100 bp
8868 11585: contig of 2718 bp in length

estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

NsII				BgIII				EcoRI			
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474	<1300	123	<1300	<1300	541	<1300					
1701	1668	6235	6101	6101	3842	3963					
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476	<1300	5194	4921	4921	2022	1983					
24	<1300	5134	5144	5144	2577	2618					
938	<1300	4119	4127	4127	10579	10596					
468	<1300	2018	2003	2003	2000	1983					
1406	1407	1230	1201	1201	177	<1300					
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2054	2080	1415	1399	1399	990	<1300					
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1781	1800	6184	6101	3113	3220
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1990	1946	3032	3064	1958	1983
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221	<1300	3435	3435	2307	2270
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		384	<1300	229	<1300
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GenCore version 5.1.4_p5_4578
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Run on: February 15, 2003, 23:10:43 ; Search time 67 Seconds
(without alignments)
1565.980 Million cell updates/sec

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Perfect score: 206
Sequence: 1 gctcgagccatgtatggac.....gcaaggtgtattatctag 206

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues
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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 100 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	31.2	15.1	876	10 US-09-393-634-65	Sequence 65, Appl
C 4	29.6	14.4	335	10 US-09-770-791-917	Sequence 917, App
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8	28.6	13.9	339	10 US-09-983-965-9	Sequence 9, Appli
9	28.6	13.9	396	9 US-09-970-966-77	Sequence 77, Appl
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C 14	28.2	13.7	14955	10 US-09-961-527A-1	Sequence 1, Appli
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C 16	27.6	13.4	308	10 US-09-294-093B-3593	Sequence 3593, Ap
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	26	27.2	13.2	3540	10	US-09-962-805-5	Sequence 5, Appli
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	28	27	13.1	460	10	US-09-864-761-3995	Sequence 3995, App
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C	30	26.6	12.9	1133	9	US-09-822-846-451	Sequence 451, App
C	31	26.6	12.9	1507	9	US-09-989-442-81	Sequence 81, Appl
C	32	26.6	12.9	2910	10	US-09-842-552-88	Sequence 88, Appl
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	91	26	12.6	2095	9	US-10-176-993-161	Sequence 161, App
	92	26	12.6	2095	9	US-10-184-658-161	Sequence 161, App


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Matches 59; Conservative 0; Mismatches 50; Indels 0;
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RESULT 8
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; Sequence 9, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 9
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 01-BOVMS1-021-Q1-E1-A9
US-09-983-965-9

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RESULT 9
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; Sequence 77, Application US/09970966
; Patent No. US20020173638A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 396
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; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: 63, 66, 81, 83, 89, 107, 115, 118, 147, 151, 190, 232, 275,
; LOCATION: 288, 294, 304, 323, 332, 369, 392
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US-09-970-966-77

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QY 96 GATACAATTTGGTGGATTGGCAACAACAACTTCCTGTGACTAACAGGTCCATAGTT 150
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RESULT 10
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; Sequence 77, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-77

Query Match 13.9%; Score 28.6; DB 10; Length 396;
Best Local Similarity 50.4%; Pred. No. 2.5;
Matches 58; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 36 GTCAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAAGCAACGC 95
Db 74 GTTAAATNCNGGACNCCTTACAATTGTGTAAANAACATGCNCANAAACATATGCATATA 133

QY 96 GATACAATTTGGTGGATTGGCAACAACAACTTCCTGTGACTAACAGGTCCATAGTT 150
Db 134 ACTACTATACAGGNGATNTGCAAAAACCCCTACTGGGAATCCATTTCATTAGTT 188

RESULT 11
US-09-738-626-2176
; Sequence 2176, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2176
; LENGTH: 3012

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2176

Query Match      13.8%; Score 28.4; DB 9; Length 3012;
Best Local Similarity 60.3%; Pred. No. 6.8;
Matches 47; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GCTCGAGCCATGGTATGGAGCTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATT 60
   |||||
Db 1598 GCATTACCCAGGCGCATTTGGTGCATACCAGGTCAAGTAAATGTCGAGGACACTGAGCGCA 1657
   |||||

QY 61 CGGTCCAAGAACAGGATA 78
   |||||
Db 1658 CGATCACCTTCCTGGATA 1675
   |||||

RESULT 12
US-09-991-980-2/c
; Sequence 2, Application US/09991980
; Patent No. US20020119543A1
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hiroyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis
; TITLE OF INVENTION: Retinol
; TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
; FILE REFERENCE: LUD 5601
; CURRENT APPLICATION NUMBER: US/09/991,980
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/880,427
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 6330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5357, 5448
; OTHER INFORMATION: nucleotide not determined
US-09-991-980-2

Query Match      13.7%; Score 28.2; DB 10; Length 6330;
Best Local Similarity 64.6%; Pred. No. 11;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 38 CAATTTCCAGGACACAGATGATTCCGTCCAAGAACAGGATAATAGAACTAAGCAACGCGA 97
   |||||
Db 4545 CCACTGCCCTGGCACAGATGTAGAAATCCAAGTATAGGTTAGGAGCACGAAGGAGGGA 4486
   |||||

QY 98 TACAA 102
   |||||
Db 4485 TAAAA 4481
   |||||

RESULT 13
US-09-961-527A-6/c
; Sequence 6, Application US/09961527A
; Patent No. US20020142324A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Turgeon, B. Gillian
; APPLICANT: Yoder, Olen
; APPLICANT: Wu, Jiansuo
; TITLE OF INVENTION: Fungal target genes and methods to identify those genes
; FILE REFERENCE: TM0129-UT
; CURRENT APPLICATION NUMBER: US/09/961,527A
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/234,673
```

```
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/234,650
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 6
; LENGTH: 8091
; TYPE: DNA
; ORGANISM: Cochliobolus
US-09-961-527A-6

Query Match      13.7%; Score 28.2; DB 10; Length 8091;
Best Local Similarity 54.3%; Pred. No. 12;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 20 CGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCCGTCCAAGAACAGGATAA 79
   |||||
Db 5642 CGTAGAAGAGATCTGGGTGTCGGACCAAGAAATTGAAGATGCTCATCAACTGCTGTAGAT 5583
   |||||

QY 80 TAGAACTAAGCAACGCCGATACAATTTGGTGGATTGGCAACAAAC 124
   |||||
Db 5582 TAGAACTCTCCTCTGAGAGAAATCTTGGCGAGGGAATTGAATCCAGC 5538
   |||||

RESULT 14
US-09-961-527A-1/c
; Sequence 1, Application US/09961527A
; Patent No. US20020142324A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Turgeon, B. Gillian
; APPLICANT: Yoder, Olen
; APPLICANT: Wu, Jiansuo
; TITLE OF INVENTION: Fungal target genes and methods to identify those genes
; FILE REFERENCE: TM0129-UT
; CURRENT APPLICATION NUMBER: US/09/961,527A
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/234,673
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/234,650
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 1
; LENGTH: 14955
; TYPE: DNA
; ORGANISM: Cochliobolus
US-09-961-527A-1

Query Match      13.7%; Score 28.2; DB 10; Length 14955;
Best Local Similarity 54.3%; Pred. No. 16;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 20 CGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCCGTCCAAGAACAGGATAA 79
   |||||
Db 12487 CGTAGAAGAGATCTGGGTGTCGGACCAAGAAATTGAAGATGCTCATCAACTGCTGTAGAT 12428
   |||||

QY 80 TAGAACTAAGCAACGCCGATACAATTTGGTGGATTGGCAACAAAC 124
   |||||
Db 12427 TAGAACTCTCCTCTGAGAGAAATCTTGGCGAGGGAATTGAATCCAGC 12383
   |||||

RESULT 15
US-09-827-864-23/c
; Sequence 23, Application US/09827864
; Patent No. US20020009458A1
; GENERAL INFORMATION:
; APPLICANT: COLAU, DIDIER
; APPLICANT: ROOS, JOEL
; TITLE OF INVENTION: RECOMBINANT DNA SEQUENCES, MOLECULES,
; VECTORS AND VACCINES FOR FELINE
; CALICIVIRUS DISEASE AND METHODS FOR
; PRODUCING AND USING SAME
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: MCDERMOTT, WILL & EMERY
STREET: 1850 K STREET, N.W., SUITE 500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/827,864
FILING DATE: 06-Apr-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GADIANO, WILHELM F
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 37712-213
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 778-8373
TELEFAX: (202) 778-8335
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-827-864-23

```
Query Match      13.6%; Score 28; DB 10; Length 2007;
Best Local Similarity 56.5%;
Pred. NO. 7.8;
Matches 52; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
```

Qy	68	AGAACAGGATAATAGAACTAAGCAACCGGATACAATTTGGGTGGATTTGGCAACAACATTC	127
Db	113	ATAAGAGGGTTATCACAAAAGCCACAGAAAGGAATTTGTTGGGGTTGACAACTAATCTA	54
Qy	128	CTGTGACTAACAGGTCATAGTTTTTCAACGAC	159
Db	53	AAGTGGGGATCCCAGCCATAGTATTTTAAGCAC	22

RESULT 16

US-09-294-093B-3593/c

; Sequence 3593, Application US/09294093B

; Patent No. US20010051335A1

; GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath, V.

; APPLICANT: Ito, Laura, Y.

; APPLICANT: Sherman, Bradley, K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

; FILE REFERENCE: PL-0009 US

; CURRENT APPLICATION NUMBER: US/09/294,093B

; CURRENT FILING DATE: 1999-04-16

; PRIOR APPLICATION NUMBER: 60/082,567

; PRIOR FILING DATE: April 21, 1998

; NUMBER OF SEQ ID NOS: 6207

; SOFTWARE: PERL Program

; SEQ ID NO 3593

; LENGTH: 308

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20010051335A1 700380551H1

; NAME/KEY: unsure

; LOCATION: 108-109, 114, 117, 124, 133-134, 139, 141, 151, 161, 167, 176, 179,

; OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-3593

```

Query Match      13.4%; Score 27.6; DB 10; Length 308;
Best Local Similarity 51.4%; Pred. No. 4.9;
Matches 54; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 72 CAGGATAATAGAACTAAGCAACGCGATACACAATTGGGTGGATTGGCAACAAACTTCCTGT 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 CNNGAAGTTGGNCCTCAANGANGGCGCANNCACTTAGGAGTTTTTGGGAAGCAAAATATCTTTA 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 132 GACTAACAGGTCCATAGTTTTTTCACGACACTTCCAAGGACGCCAT 176
    - ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 AAAACACATGTTCTTTAAAGCTCACACCCCTTCCCATAAATCCAT 31
    - ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 17
US-09-978-199-1
; Sequence 1, Application US/09978199
; Patent No. US20020104126A1
; GENERAL INFORMATION:
; APPLICANT: POGUE, GREGORY P.
; APPLICANT: VELICHKO, SHARLENE
; TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
; FILE REFERENCE: 42202
; CURRENT APPLICATION NUMBER: US/09/978,199
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/240,967
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Bovine sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(441)
US-09-978-199-1

```

	Query Match	13.4%;	Score 27.6;	DB 10;	Length 444;
	Best Local Similarity	58.5%;	Pred. No. 5.7;		
	Matches 48; Conservative	0;	Mismatches 34;	Indels 0;	Gaps 0;
QY	69 GAACAGGATAATAGAACTAAGCAACGGCATACAATTGGGTGGATTGGCAACAACACTTCC				
Ddb	340 GCAAAGCATTATTGCAGTGAGCAAGGCATTACACCCTGGGTGGCATGGAAAAGTCATTGT				
QY	129 TGTGACTAACAGGTCCATAGTTT				
Ddb	400 CGAGACCATGACCGTCAGCAGTT				

RESULT 18

US-09-879-536-653/c

; Sequence 653, Application US/09879536

; Patent No. US2002014298A1

; GENERAL INFORMATION:

; APPLICANT: Endege, Wilson O.

; APPLICANT: Steinmann, Kathleen E.

; APPLICANT: Astle, Jon H.

; APPLICANT: Burgess, Christopher C.

; APPLICANT: Bushnell, Steven E.

; APPLICANT: Carroll III, Eddie

; APPLICANT: Catino, Theodore J.

; APPLICANT: Derti, Adnan

; APPLICANT: Ford, Donna M.

; APPLICANT: Lewis, Marcia E.

; APPLICANT: Monahan, John E.

; APPLICANT: Schlegel, Robert

; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

; TITLE OF INVENTION: PRODUCTS

; FILE REFERENCE: CCD-257 (US)

; CURRENT APPLICATION NUMBER: US/09/879,536

; CURRENT FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: US 60/088,801

```

; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 653
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-536-653

```

Query Match	13.4%;	Score 27.6;	DB 10;	Length 468;
Best Local Similarity	55.1%;	Pred. No. 5.8;		
Matches 54;	Conservative	0;	Mismatches 44;	Indels 0;
				Gaps 0;

[illegible]

RESULT 19
US-10-046-935-939/c
; Sequence 939, Application US/10046935
; Patent No. US2002015601A1
; GENERAL INFORMATION:

```

; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 939
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n = A, T, C or G
US-10-046-935-939

```

Query Match 13.4%; Score 27.6; DB 9; Length 500;
Best Local Similarity 56.7%; Pred. No. 6;
Matches 51; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

[illegible]

RESULT 20
US-09-878-178-939/c
; Sequence 939, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527

```

; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 939
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(500)
; OTHER INFORMATION: n = A,T,C or G
US-09-878-178-939

```

Query Match	13.4%;	Score 27.6;	DB 9;	Length 500;
Best Local Similarity	56.7%;	Pred. No. 6;		
Matches 51; Conservative	0;	Mismatches 39;	Indels 0;	Gaps 0;

Qy	34	TGGTCAATTCCAGGACACAGATGATTCCGTC	CAAGAACAGGATAATAAGCAAC	93
Db	363	TCGTCAATTCCTTTCAAAGATTAGATGGATCA	TATAAAGGAGAACTGAGGAAACAAGC	304

Qy 94 GCGATACAATTTGGTGGATTGGCAACAAA 123
Db 303 TCTAGATCATTTTAAATGCTGAGGGATCAGA 274

RESULT 21
US-09-938-842A-5349
; Sequence 5349, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 5349
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-5349

Query Match	13.4%;	Score 27.6;	DB 9;	Length 2000;
Best Local Similarity	56.7%;	Pred. No. 11;		
Matches 51;	Conservative	0;	Mismatches 39;	Indels 0;
				Gaps 0;

Qy 64 TCCAAGAACAGGATAAATAGAACTAAGCAACGGCATACAATTTGGTGGATTGGCAACAAA 123

Db 1170 TCAGATATTTGGGTAAAAATATTCCAGGTATTTAGATAAAAAATTTAGATATTTTCGGCTATAAA 1229

QY 124 CTTCTGTGACTAACAGGTCCATAGTTTTT 153
| | | | | | | | | | | | | | | | | | | | | |
Db 1230 ATACCTGAATCTCAAGATACCCATTTTTT 1259

RESULT 22
US-09-978-199-3
; Sequence 3, Application US/09978199
; Patent No. US20020104126A1
; GENERAL INFORMATION:
; APPLICANT: POGUE, GREGORY P.

APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
FILE REFERENCE: 42202
CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 10132
TYPE: DNA
ORGANISM: Bovine sp.
US-09-978-199-3

Query Match 13.4%; Score 27.6; DB 10; Length 10132;
Best Local Similarity 58.5%; Pred. No. 21;
Matches 48; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 69 GAACAGGATAATAGAACTAAGCAACGCCGATACAAATTTGGTGGATTGGCAACAACTTCC 128
Db 6106 GCAAAGCATATTGTCAGTGAGCAAGGCATTACAGCCTGGGTGGCATGGAAAAAGTCATTGT 6165
QY 129 TGTGACTAACAGGTCCATAGTT 150
Db 6166 CGAGACCATGACGTCAGCAGTT 6187

RESULT 23
US-09-864-761-16642
Sequence 16642, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 16642
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007869.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.87
US-09-864-761-16642

Query Match 13.3%; Score 27.4; DB 10; Length 480;
Best Local Similarity 57.6%; Pred. No. 6.9;
Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 34 TGGTCAATTTCCAGGACACAGATGATTTCGGTCCCAAGAACAGGATAATAGAACTAAGCAAC 93
Db 363 TGCCGAGTTACTGGGAGCTGTAAAGTTCCGGTCAAACCAGACCAGATGAGAACCATATAAAC 422
QY 94 GCGATACAAATTTGGGTGGATTGGCA 118
Db 423 CCGATGCCTCTTGGGAGGTTTGACA 447

RESULT 24
US-09-864-761-8383
Sequence 8383, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 8383
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL158845.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
US-09-864-761-8383

Query Match 13.3%; Score 27.4; DB 10; Length 586;
Best Local Similarity 55.9%; Pred. No. 7.5;
Matches 52; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 22 TATACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATA 81
Db 268 TTCCAGGCTCTTGAGCCATTGCCAATGGTCTGCTCATCTGGTCAAGAACACACCAAT 327

QY 82 GAACTAAGCAACGCCGATACAAATTTGGTGGATT 114
Db 328 TCAGTAACCAAGTCATCCCTTTGGGGTAAAT 360

RESULT 25
US-09-867-701-415
; Sequence 415, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 415
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(391)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-415

Query Match 13.2%; Score 27.2; DB 10; Length 391;
Best Local Similarity 72.9%; Pred. No. 7.4;
Matches 35; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 120 CAAACTTCCTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAA 167
Db 74 CCACCTTCCTGTGGCTAACAGGTTCTTGAATTTCAATACAGATGCAA 121

RESULT 26
US-09-962-805-5
; Sequence 5, Application US/09962805
; Patent No. US20020058313A1
; GENERAL INFORMATION:

; APPLICANT: RENKONEN, Risto
; APPLICANT: MATTILA, Pirkko
; APPLICANT: HIRVAS, Laura
; APPLICANT: HORTLING, Solveing
; APPLICANT: KALLIOINEN, Tuula
; APPLICANT: KAURANEN, Sirkka-Liisa
; APPLICANT: JAERVINEN, Nina
; APPLICANT: MAEKI, Minna
; APPLICANT: NIITYMAEKI, Jaana
; APPLICANT: RAEBINAE, Jarkko
; TITLE OF INVENTION: USE OF RECOMBINANT ENZYMES FOR PREPARING GDP-L-FUCOSE AND FUCOSYL
; TITLE OF INVENTION: GLYCANS
; FILE REFERENCE: 2242/50463
; CURRENT APPLICATION NUMBER: US/09/962,805
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FI 20002114
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 3540
; TYPE: DNA
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2492)..(2492)
; OTHER INFORMATION: unknown
US-09-962-805-5

Query Match 13.2%; Score 27.2; DB 10; Length 3540;
Best Local Similarity 50.8%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 70 AACAGGATAATAGAACTAAGCAACGCCGATACAAATTTGGTGGATTGGCAACAACTTCCT 129
Db 2148 AACATAACATATCTTTAAGCTTTTCTATCTCTTTTGGAAATTTGGACCAATAAAATCT 2207

QY 130 GTGACTAACAGGTCCATAGTTTTTTCACGACACTTCCAAAGGACGCCATACCCGAAACAAAGCA 189
Db 2208 AGGTGATATTGGAGGATGGTATTGTCTCAACTTCTCATAGTGAGACACCCCGTACAAAACA 2267

QY 190 AGGTGTTA 197
Db 2268 TGGTTTA 2275

RESULT 27
US-10-176-640-1/c
; Sequence 1, Application US/10176640
; Publication No. US20030023056A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: GENES ENCODING MYCOBACTERIAL PROTEINS ASSOCIATED WITH
; TITLE OF INVENTION: CELL BINDING AND CELL ENTRY AND USES THEREOF
; FILE REFERENCE: 1038-1231 MIS
; CURRENT APPLICATION NUMBER: US/10/176,640
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 08/677,970
; PRIOR FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4739
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-176-640-1

Query Match 13.2%; Score 27.2; DB 9; Length 4739;
Best Local Similarity 56.8%; Pred. No. 21;
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 95 CGATACAATTTGGTGGATTGGCAACAAACTTCTGTGACTAACAGGTCCATAGTTTTC 154

Db 146 CGTTACAATTTCTGTGCGATTTTCCCTTCTCTCCGTGAACCCAGCTGATGCAGAACGTCTT 87
QY 155 ACGACACTTCCAGGACGCCATACCGAA 182
Db 86 TCAACATTTCACACAGGCGCGTAGCGCA 59

RESULT 28
US-09-864-761-3995
; Sequence 3995, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3995
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049835.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

Query Match 13.1%; Score 27; DB 10; Length 460;
Best Local Similarity 62.7%; Pred. No. 9.3;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 62 GGTCCAAGAACAGGATAATAGAACTAAGCAACGGGATACAAATTTGGTGGATTGGCAACA 121
Db 298 GGTCCCAGAGGAGGAGAGAGAAAGCAAGAGATTATTGAGGAAACAATGCCTAAA 357
QY 122 AACTTCC 128
Db 358 AACTTCC 364

RESULT 29
US-09-770-149-989
; Sequence 989, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 989
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-989

Query Match 12.9%; Score 26.6; DB 10; Length 598;
Best Local Similarity 50.4%; Pred. No. 14;
Matches 65; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 41 TTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATATAAGCAACCGGATAC 100
Db 122 TTTATATCAAAATAGACGAAATGCCCTGTCCGGACGGCGGATACAGCAAGACGGTGA 181
QY 101 AATTTGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACA 160
Db 182 AGCTGGAGAGGTACAATAGTACTCTCCGGAAGATTTCACAGCACCAAGTTCTCAACGCTT 241
QY 161 CTTCCAAGG 169
Db 242 CTTCTAAG 250

RESULT 30
US-09-822-846-451/c
; Sequence 451, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.

```
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 451
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-846-451

Query Match      12.9%; Score 26.6; DB 9; Length 1133;
Best Local Similarity 60.3%; Pred. No. 19;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 125 TTCCTGTGACTAACAGGTCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACA 184
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1093 TTCCTGATTATAAAGTAACACAGTTTGTCTCACACACTTACAAAATAAAGATATCTAAAG 1034

QY 185 AAGCAAGGTGTTA 197
      ||||| |||||
Db 1033 GAGAAAAGAAATAA 1021

RESULT 31
US-09-989-442-81/c
; Sequence 81, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ08
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
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; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
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Qy	53	AGATGATT	CGGTCC	AAGAACA	GAGGATAA	TAGAACTA	AGACCAAC	GC	GATACAA	TTTGGGTGGA	112
Dd	1365	AGATGAAT	TCTTCT	CAAGACAA	CAGAATCAT	TCTTAAGCAA	GC	ACTCCGAT	CAGGGGCA	1308	
Qy	113	TTGGCAACA	AACT	125							
Dd	1305	ACAGCAACA	CTCT	1293							

RESULT 33
US-09-783-066-7/c
; Sequence 7, Application US/09783066
; Patent No. US20020142302A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Yang, Yonghong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020142302A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 791CIP2D
; CURRENT APPLICATION NUMBER: US/09/783,066
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: No. US20020142302A1 Yet Assigned
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/552,929
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 7
; LENGTH: 5772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)..(2125)
US-09-783-066-7

Query Match 12.9%; Score 26.6; DB 10; Length 5772;
Best Local Similarity 58.0%; Pred. No. 37;
Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 74 GGATAAATAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTTCTGTGA 133
Db 2825 GAATAATTTCTCTGAGCAACAGGTTACAATTTGCATATAAGGCAATAGAACTATAGGGA 2766

QY 134 CTAACAGGTCATAGTTTTC 154
Db 2765 GGAACAAGTTCAAATGCTTC 2745

RESULT 34
US-09-901-152-3/c
; Sequence 3, Application US/09901152
; Publication No. US20030022824A1
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001248
; CURRENT APPLICATION NUMBER: US/09/901,152
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 58985
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(58985)
; OTHER INFORMATION: n = A,T,C or G

US-09-901-152-3

Query Match 12.9%; Score 26.6; DB 9; Length 58985;
Best Local Similarity 56.2%; Pred. No. 97;
Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 7 GCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCC 66
Db 46090 GACATCCTGCGGCGTGACAGACTTTCATGGGCGCGTGCTGAACCTCCCAAGTCCCCCTCC 46031

QY 67 AAGAACAGGATAATAGAACTAAGCAACGC 95
Db 46030 CACAAAGCAGAGATAGAAATGAGACAAAGC 46002

RESULT 35
US-09-864-761-3985/c
; Sequence 3985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3985
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008012.8


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; SEQ ID NO 892
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AI171229
US-09-917-800A-892

Query Match          12.7%; Score 26.2; DB 10; Length 570;
Best Local Similarity 54.7%; Pred. No. 19;
Matches 52; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 28 AGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGAACACAGGATAATAGAACTA 87
   |||||
Db 161 AGATATGGGTTTTTCGAGAGGCCACAGGTCCACAGCTCCATGAACACAGGCGAATTGGTCCT 220
   |||||

QY 88 AGCAACGCGATACAAATTTGGGTGGATTGGCAACAA 122
   |||||
Db 221 TGCTTGGGAAATCCTCCAGGTGCTTCTCCAAAAA 255
   |||||

RESULT 39
US-09-778-900A-4
; Sequence 4, Application US/09778900A
; Publication No. US20020192647A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, JOHN C.
; TITLE OF INVENTION: DIAGNOSTIC METHOD
; FILE REFERENCE: PLS/009901/0277123
; CURRENT APPLICATION NUMBER: US/09/778,900A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: GB 0004232.5
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (878)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-778-900A-4

Query Match          12.7%; Score 26.2; DB 9; Length 1352;
Best Local Similarity 56.3%; Pred. No. 27;
Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 6 AGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
   |||||
Db 778 AGCTCTGATGATGTCAGGTAAGATTCTTTCTCAAACTTTATATACACAGAAATTTTCCAAC 837
   |||||

QY 66 CAAGAACAGGATAATAGAACTAAGCAA 92
   |||||
Db 838 AAAAAAAGAAAGAAAGAAAGAACGAAA 864
   |||||

RESULT 40
US-09-881-752A-355
; Sequence 355, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; FILE REFERENCE: Encoding No. US20020115078A1el Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
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; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 355
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1577)
US-09-881-752A-355

Query Match          12.7%; Score 26.2; DB 10; Length 1630;
Best Local Similarity 63.5%; Pred. No. 30;
Matches 40; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 106 GGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCATAGTTTTCACGACACTTCC 165
   |||||
Db 1245 GGGCGCTTTAGCACCAACATTCCTTGATGGCAAGACGATTGTTTGTGACAAATTTA 1304
   |||||

QY 166 AAG 168
   ||
Db 1305 ACG 1307

RESULT 41
US-09-938-842A-3155
; Sequence 3155, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3155
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3155

Query Match          12.7%; Score 26.2; DB 9; Length 2000;
Best Local Similarity 56.3%; Pred. No. 32;
Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 67 AAGAACAGGATAATAGAACTAAGCAACGCCGATACAAATTTGGTGGATTGGCAACAACTT 126
   |||||
Db 401 AAGAATAAGCAATAACACTAAAGCATGTTAAAGTCTTCTTGAACATTGAAATAACACAT 460
   |||||

QY 127 CCTGTGACTAACAGGTCCTCATAGTTTTT 153
   |||||
Db 461 CTCGTACAGAGCCGGTCCAACGTTTTT 487
   |||||

RESULT 42
US-10-067-385-7
; Sequence 7, Application US/10067385
; Patent No. US20020110562A1
; GENERAL INFORMATION:
; APPLICANT: Adamou, John
```

APPLICANT: Choi, Gil
; TITLE OF INVENTION: Streptococcus Pneumoniae Proteins and Vaccines
; FILE REFERENCE: 469201-589
; CURRENT APPLICATION NUMBER: US/10/067,385
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US/09/590,991
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US/60/138,453
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2319
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-067-385-7

Query Match 12.7%; Score 26.2; DB 12; Length 2319;
Best Local Similarity 53.4%; Pred. No. 34;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 99 ACAATTGGGTGGATTGGCAACAACCTCTGTGACTAACAGGTCCATAGTTTTCACGA 158
|||||
Db 390 ACACCTTGAATCTTGGAAAGATAAGTAATGTTCTAAAAATGCCAAGGTATATATGG 449
|||||

QY 159 CACTTCCAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
|||||
Db 450 GAATAACTATAAATCTATAGAAATCAAAGCGACCAAGTATGAT 492
|||||

RESULT 43
US-09-801-368-109
; Sequence 109, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 109
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-109

Query Match 12.7%; Score 26.2; DB 10; Length 3228;
Best Local Similarity 58.2%; Pred. No. 40;
Matches 46; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 21 GTATACGAGTCTTGGTCAATTCCAGGACACAGATGATTCGGTCCAGAACAGGATAAT 80
|||||
Db 2451 GTATACGAGTGGTGGCCTATTCTACCACAGAGACAAAGCAACCAAGGGGACAAAC 2510
|||||

QY 81 AGAACTAAGCAACGGGATA 99

Db 2511 AGAGCAAAACCAAGGGACA 2529
|||||
RESULT 44
US-09-905-119-1/c
; Sequence 1, Application US/09905119
; Patent No. US20020091096A1
; GENERAL INFORMATION:
; APPLICANT: Mordin, Andrew D
; APPLICANT: Oomen, Raymond P.
; APPLICANT: Dunn, Pamela L
; TITLE OF INVENTION: Chlamydia Antigens and Corresponding DNA Fragments and
; FILE REFERENCE: 19721-010 DIV
; CURRENT APPLICATION NUMBER: US/09/905,119
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/106,037
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/154,658
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/427,501
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1366)
US-09-905-119-1

Query Match 12.6%; Score 26; DB 10; Length 1550;
Best Local Similarity 57.3%; Pred. No. 34;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 122 AACTTCTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAAAGGACGCCATACCGA 181
|||||
Db 1085 AACGTACTGTGGCAGACCAAGTCTCCAGCTTTTCTGAGTCCCTTAAAGTTCTCTCCATAA 1026
|||||

QY 182 ACAAGCAAGGTGTTATTATCC 203
|||||
Db 1025 ACCAAGTAGGTTTCTTTTCC 1004
|||||

RESULT 45
US-09-739-451-9
; Sequence 9, Application US/09739451
; Patent No. US20010024813A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Dendriac and Brainiac-3
; FILE REFERENCE: PF464
; CURRENT APPLICATION NUMBER: US/09/739,451
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/213,364
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/077,687
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/108,928
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-739-451-9

Query Match 12.6%; Score 26; DB 10; Length 1773;
Best Local Similarity 50.0%; Pred. No. 36;

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Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 75 GATAATAGAACTAAGCAACGCGATACATACTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 252 GATGTGAAGCCAGGAGCCATTAGAGTTACTTGGGTGAAAAAAGTCTTGGTGGGA 311
QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAAGGACGCCATACCGAACAAGCAAGTG 194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 312 TATGAGGTTCTTACATTTTCTTATTAGCCCAAGGCTGAAAAGGAACAAATGTTG 371
QY 195 TTATTATCCT 204
    ||| |||
Db 372 GCATTGTCCT 381
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RESULT 46

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US-09-992-598-208
; Sequence 208, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
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; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
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;	PRIOR FILING DATE:	1998-06-18
;	PRIOR APPLICATION NUMBER:	60/089947
;	PRIOR FILING DATE:	1998-06-19
;	PRIOR APPLICATION NUMBER:	60/089948
;	PRIOR FILING DATE:	1998-06-19
;	PRIOR APPLICATION NUMBER:	60/089952
;	PRIOR FILING DATE:	1998-06-19
;	PRIOR APPLICATION NUMBER:	60/090246
;	PRIOR FILING DATE:	1998-06-22
;	PRIOR APPLICATION NUMBER:	60/090252
;	PRIOR FILING DATE:	1998-06-22
;	PRIOR APPLICATION NUMBER:	60/090254
;	PRIOR FILING DATE:	1998-06-22
;	PRIOR APPLICATION NUMBER:	60/090349
;	PRIOR FILING DATE:	1998-06-23
;	PRIOR APPLICATION NUMBER:	60/090355
;	PRIOR FILING DATE:	1998-06-23
;	PRIOR APPLICATION NUMBER:	60/090429
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090431
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090435
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090444
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090445
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090472
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090535
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090540
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090542
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090557
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090676
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090678
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090690
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090694
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090695
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090696
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090862
;	PRIOR FILING DATE:	1998-06-26
;	PRIOR APPLICATION NUMBER:	60/090863
;	PRIOR FILING DATE:	1998-06-26
;	PRIOR APPLICATION NUMBER:	60/091360
;	PRIOR FILING DATE:	1998-07-01
;	PRIOR APPLICATION NUMBER:	60/091478
;	PRIOR FILING DATE:	1998-07-02
;	PRIOR APPLICATION NUMBER:	60/091544
;	PRIOR FILING DATE:	1998-07-01
;	PRIOR APPLICATION NUMBER:	60/091519
;	PRIOR FILING DATE:	1998-07-02
;	PRIOR APPLICATION NUMBER:	60/091626
;	PRIOR FILING DATE:	1998-07-02
;	PRIOR APPLICATION NUMBER:	60/091633
;	PRIOR FILING DATE:	1998-07-02
;	PRIOR APPLICATION NUMBER:	60/091978
;	PRIOR FILING DATE:	1998-07-07
;	PRIOR APPLICATION NUMBER:	60/091982
;	PRIOR FILING DATE:	1998-07-07
;	PRIOR APPLICATION NUMBER:	60/092182
;	PRIOR FILING DATE:	1998-07-09

;	PRIOR APPLICATION NUMBER: 60/089900
;	PRIOR FILING DATE: 1998-06-18
;	PRIOR APPLICATION NUMBER: 60/089947
;	PRIOR FILING DATE: 1998-06-19
;	PRIOR APPLICATION NUMBER: 60/089948
;	PRIOR FILING DATE: 1998-06-19
;	PRIOR APPLICATION NUMBER: 60/089952
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;	PRIOR FILING DATE: 1998-06-22
;	PRIOR APPLICATION NUMBER: 60/090252
;	PRIOR FILING DATE: 1998-06-22
;	PRIOR APPLICATION NUMBER: 60/090254
;	PRIOR FILING DATE: 1998-06-22
;	PRIOR APPLICATION NUMBER: 60/090349
;	PRIOR FILING DATE: 1998-06-23
;	PRIOR APPLICATION NUMBER: 60/090355
;	PRIOR FILING DATE: 1998-06-23
;	PRIOR APPLICATION NUMBER: 60/090429
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090431
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090435
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090444
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090445
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090472
;	PRIOR FILING DATE: 1998-06-24
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;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090540
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090542
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090557
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090676
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090678
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090690
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090694
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090695
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090696
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090862
;	PRIOR FILING DATE: 1998-06-26
;	PRIOR APPLICATION NUMBER: 60/090863
;	PRIOR FILING DATE: 1998-06-26
;	PRIOR APPLICATION NUMBER: 60/091360
;	PRIOR FILING DATE: 1998-07-01
;	PRIOR APPLICATION NUMBER: 60/091478
;	PRIOR FILING DATE: 1998-07-02
;	PRIOR APPLICATION NUMBER: 60/091544
;	PRIOR FILING DATE: 1998-07-01
;	PRIOR APPLICATION NUMBER: 60/091519
;	PRIOR FILING DATE: 1998-07-02
;	PRIOR APPLICATION NUMBER: 60/091626
;	PRIOR FILING DATE: 1998-07-02
;	PRIOR APPLICATION NUMBER: 60/091633
;	PRIOR FILING DATE: 1998-07-02
;	PRIOR APPLICATION NUMBER: 60/091978
;	PRIOR FILING DATE: 1998-07-07
;	PRIOR APPLICATION NUMBER: 60/091982
;	PRIOR FILING DATE: 1998-07-07
;	PRIOR APPLICATION NUMBER: 60/092182
;	PRIOR FILING DATE: 1998-07-09

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Query Match      12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGGGATACAAATTTGGTGGATTGGCAACAACAACTTCTGTGAC 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 GATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGTGAAAAAAGTCTTGGTGGGA 648

QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAGCAAGGTG 194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 TATGAGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTG 708

QY 195 TTATTATCCT 204
    ||| ||| |||
Db 709 GCATTGTCCT 718
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RESULT 48
US-10-063-547-35
; Sequence 35, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 35
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-35
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Query Match      12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGGGATACAAATTTGGTGGATTGGCAACAACAACTTCTGTGAC 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 GATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGTGAAAAAAGTCTTGGTGGGA 648

QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAGCAAGGTG 194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 TATGAGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTG 708

QY 195 TTATTATCCT 204
    ||| ||| |||
Db 709 GCATTGTCCT 718
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RESULT 49
US-09-989-735-208
; Sequence 208, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
```

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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
```


APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/066770
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
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;	PRIOR APPLICATION NUMBER: 60/089538
;	PRIOR FILING DATE: 1998-06-17
;	PRIOR APPLICATION NUMBER: 60/089598
;	PRIOR FILING DATE: 1998-06-17
;	PRIOR APPLICATION NUMBER: 60/089599
;	PRIOR FILING DATE: 1998-06-17
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;	PRIOR FILING DATE: 1998-06-23
;	PRIOR APPLICATION NUMBER: 60/090355
;	PRIOR FILING DATE: 1998-06-23
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;	PRIOR FILING DATE: 1998-06-24
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;	PRIOR FILING DATE:	1998-07-07
;	PRIOR APPLICATION NUMBER:	60/092182
;	PRIOR FILING DATE:	1998-07-09

Query Match 12.6% Score 26; DB 9; Length 2095;

Best Local Similarity 50.0%; Pred. No. 39;

Matches	65;	Conservative	0;	Mismatches	65;	Indels	0;	Gaps	0;
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75 GATAATAGAACTAAGCAACGCGATACAATTGGGTGGATTGGCAACAACTTCCTGTGAC 134

Db 589 GATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCTTGTGGGGA 648

135 TAA CAGGTC CATTAGTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTG 194

649 TATGACGTTCTTACATTTTCTTATTAGGCAAGAGGCTGAAAAGGAAGACAAAATGTTG 708

Q. 103. What is the difference between a proton and a neutron?

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RESULT 56

US-09-997-653-208

03-03-207 033 200
: sequence 208, Application US/09997653

; Publication No. US20030008297A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-04-28
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PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431


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; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 161
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-161

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	Query Match	12.6%;	Score 26;	DB 9;	Length 2095;
	Best Local Similarity	50.0%;	Pred. No. 39;		
Matches	65; Conservative	0;	Mismatches	65;	Indels 0; Gaps
QY	75	GATAATAGRACTAAGCAACGCGATACAATTGGGTGGATTGGCAACAAACTTCCTGTGAC	134		
Db	589	GATGTGAAGCCAGGCAGGCCATTACAGTTACTTGGGGTGAAAAAAGCTCTTGGTGGGGA	648		
QY	135	TAACAGGTCCATAGTTTTTCACGCACATTCCAAAGCAGCCATACCGAACAAAGCAAGGTG	194		
Db	649	TATGAGGTCTTACATTTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTG	708		
QY	195	TTATTATCCT	204		
Db	709	GCATTGTCTT	718		

APPLICANT:	Eaton, Paul L.
APPLICANT:	Ferraro, Napoleone
APPLICANT:	Fong, Sherman
APPLICANT:	Gerber, Hanspeter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, J. Christopher
APPLICANT:	Gurney, Austin L.
APPLICANT:	Kljavin, Ivar J.
APPLICANT:	Napier, Mary A.
APPLICANT:	Pañ, James
APPLICANT:	Paoni, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tumas, Daniel
APPLICANT:	Watanabe, Colin K.
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William I.
APPLICANT:	Zhang, Zemin

```

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C4
; CURRENT APPLICATION NUMBER: US/09/993,667
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311

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/	PRIOR FILING DATE: 1998-06-17
/	PRIOR APPLICATION NUMBER: 60/089801
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/	PRIOR APPLICATION NUMBER: 60/091360
/	PRIOR FILING DATE: 1998-07-01
/	PRIOR APPLICATION NUMBER: 60/091478


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; SEQ ID NO 161
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-738-161

Query Match      12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 GATGTGAAGCCAGGCGCCATTAGAGTTACTTTGGGTGAAAAAAGTCTTGGTGGGA 648

QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAAAGGACGCCATACCGAACAAGCAAGGTG 194
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Db 649 TATGAGGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAAGGAACAAAATGTTG 708

QY 195 TTATTATCCT 204
    ||| ||| |||
Db 709 GCATTGTCCT 718

RESULT 65
US-10-175-752-161
; Sequence 161, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 161
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-752-161

Query Match      12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 GATGTGAAGCCAGGCGCCATTAGAGTTACTTTGGGTGAAAAAAGTCTTGGTGGGA 648

QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAAAGGACGCCATACCGAACAAGCAAGGTG 194
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 TATGAGGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAAGGAACAAAATGTTG 708

QY 195 TTATTATCCT 204
    ||| ||| |||
Db 709 GCATTGTCCT 718

RESULT 66
US-10-176-482-161
; Sequence 161, Application US/10176482
; Publication No. US20030022296A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT APPLICATION NUMBER: US/10/176,482
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 161
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-482-161

Query Match      12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
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Db 589 GATGTGAAGCCAGGCGCCATTAGAGTTACTTTGGGTGAAAAAAGTCTTGGTGGGA 648

QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAAAGGACGCCATACCGAACAAGCAAGGTG 194
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 TATGAGGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAAGGAACAAAATGTTG 708

QY 195 TTATTATCCT 204
    ||| ||| |||
Db 709 GCATTGTCCT 718

RESULT 67
US-10-176-757-161
; Sequence 161, Application US/10176757
; Publication No. US20030022297A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C86
; CURRENT APPLICATION NUMBER: US/10/176,757
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 161
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-757-161

Query Match      12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
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Db 649 TATGAGGTTCTTACATTTTCTTATTAGCCCAAGAGGCTGAAAAGGAAGCAAAATGTTG 708

Qy 195 TTATTATCCT 204

|||||

Db 709 GCATTGTCCT 718

RESULT 71

US-09-990-438-208

; Sequence 208, Application US/09990438

; Publication No. US20030027754A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C3

; CURRENT APPLICATION NUMBER: US/09/990,438

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

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; PRIOR APPLICATION NUMBER: 60/087609

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; PRIOR APPLICATION NUMBER: 60/087759

; PRIOR FILING DATE: 1998-06-02

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; PRIOR APPLICATION NUMBER: 60/088029

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088030

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; PRIOR FILING DATE: 1998-06-04

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; PRIOR FILING DATE: 1998-06-04

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; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/088655

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: 60/088734

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; PRIOR APPLICATION NUMBER: 60/088738

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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 12.6%; Score 26; DB 9; Length 2095;

Best Local Similarity 50.0%; Pred. No. 39;

Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACCGGATACAACTTGGGTGGATTGGCAACAACTTCTGTGAC 134

Db 589 GATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGTGAAAAAAGTCTTGGTGGGA 648

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;	PRIOR FILING DATE: 1998-07-09

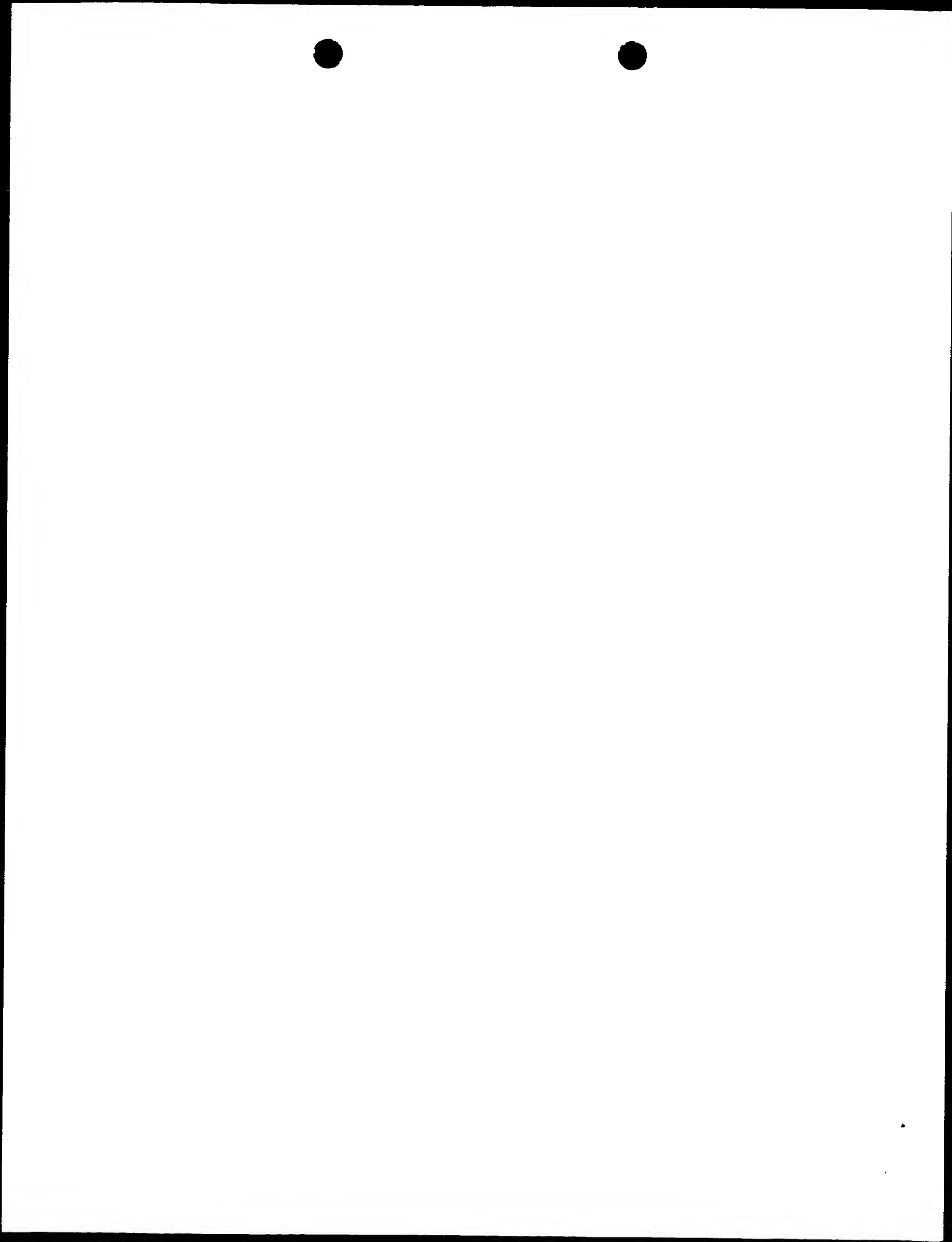
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QY 135 TAACAGGTCATAGTTTTCACGACACTTCCAAAGGACGCCATACCGAACAAAGCAAGGTG 194
Db 649 TATGAGGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAAATGTTG 708
QY 195 TTATTATCCT 204
Db 709 GCATTGTCCT 718

RESULT 75
US-10-173-700-161
; Sequence 161, Application US/10173700
; Publication No. US20030027262A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C14
; CURRENT APPLICATION NUMBER: US/10/173,700
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 161
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-700-161

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 75 GATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAACTTCTGTGAC 134
Db 589 GATGTGAAGCCAGGCGCCATTAGAGTTACTTGGGGTGAAGAAAAAGTCTTGGTGGGA 648
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Db 649 TATGAGGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAAATGTTG 708
QY 195 TTATTATCCT 204
Db 709 GCATTGTCCT 718

Search completed: February 16, 2003, 00:53:11
Job time : 1273 secs



GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 21:13:02 ; Search time 194 Seconds
(without alignments)
2391.297 Million cell updates/sec

Title: 09-833799-13C
Perfect score: 206
Sequence: 1 gctcgagccatggtatggac.....gcaaggtgtattatcctag 206

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :				N Geneseq 101002:*			
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				3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT.*			
				4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT.*			
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				24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT.*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	37.6	18.3	1101	21 AAC53703	Arabidopsis thalia
C 2	37.6	18.3	1593	21 AAC49057	Arabidopsis thalia
C 3	37.6	18.3	1622	21 AAC39118	Arabidopsis thalia
C 4	32.6	15.8	831	20 AAX37428	Human secreted pro
C 5	31.2	15.1	876	22 AAF92516	Human T2R16 nucleo
C 6	30.8	15.0	15165	23 ABL20844	Drosophila melanog
C 7	30.2	14.7	325791	22 AAS43104	Human Oestrogen re
C 8	29.6	14.4	335	24 ABQ86047	Arabidopsis thalia
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85 27.6 13.4 964 10 AAN92057
86 27.6 13.4 964 14 AAQ39092
87 27.6 13.4 964 20 AAV08922
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C 93 27.6 13.4 3975 21 AAC51553
94 27.6 13.4 10130 24 AAD39129
95 27.4 13.3 480 22 AAI02935
96 27.4 13.3 586 22 ABA62594
97 27.4 13.3 586 22 ABA29917
98 27.4 13.3 586 22 AAK10953
99 27.4 13.3 586 22 AAI17657
100 27.4 13.3 1655 21 AAZ51554

Arabidopsis thalia
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ss sequence of cDN
Bovine lysozyme c
Bovine Lysozyme c2
Arabidopsis thalia
Human breast tumou
Human prostate exp
Human prostate exp
Human thyroglobuli
Arabidopsis thalia
p1044-Bolys plasmi
Probe #2926 used t
Human foetal liver
Probe #8383 for ge
Human brain expres
Probe #7590 for ge
Human hypoxia resp

ALIGNMENTS

RESULT 1

AAC53703/c

ID AAC53703 standard; DNA; 1101 BP.

XX AC AAC53703;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 75420.

XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.
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Best Local Similarity 53.4%; Pred. No. 0.015;
Matches 79; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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Db 1014 GACTCATTTATATGATCACATATATAAGAAAGGTGTGAGCCGCATCACATAGCCTATGGT 955

QY 65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAAC 124
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QY 125 TTCCTGTGACTAACAGGTCCTATGTTT 152
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RESULT 3
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ID AAC39118 standard; DNA; 1622 BP.
XX AC AAC39118;
XX XX
DT 17-OCT-2000 (first entry)
XX XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 23436.
XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX XX
PD 06-SEP-2000.
XX XX
PF 25-FEB-2000; 2000EP-0301439.
XX XX
PR 25-FEB-1999; 99US-0121825.
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DR WPI; 1999-190160/16.
DR P-PSDB: AAY07803.

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XX New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1a; Page 224; 280pp; English.
XX
CC This invention describes novel isolated human secreted proteins and
CC their encoding nucleic acid sequences. The products of the invention
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also pathological conditions can be
CC diagnosed by determining the presence or amount of expression of
CC the new polypeptides in a sample or by determining the presence or
CC absence of mutations in the new polynucleotides. Specific uses are
CC described for each of the 70 polynucleotides, based on which tissues
CC they are most highly expressed in, and include developing products for
CC the diagnosis or treatment of cancer, tumours, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC asthma, sepsis, diabetes, Alzheimer's and cognitive disorders,
CC schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine
CC disorders, infections and AIDS. The human secreted proteins of the
CC invention are represented in AAY07744-Y07850 and the encoding nucleic
CC acids are represented in AAX37369-X37441.
XX
SQ Sequence 831 BP; 273 A; 125 C; 163 G; 267 T; 3 other;

Query Match          15.8%; Score 32.6; DB 20; Length 831;
Best Local Similarity 57.3%; Pred. No. 0.61;
Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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QY 79 ATAGAACTAAGCAACGGCATACAATTTGGTGGATTGGCAACA 121
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AC
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XX 16-MAY-2001 (first entry)
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XX Human T2R16 nucleotide sequence SEQ ID NO:31.
XX
XX Human; rat; mouse; T2R; taste receptor; G-protein coupled receptor;
KW taste transduction G-protein coupled receptor; identification; tongue;
KW taste sensory neuron; taste cell; taste modulator; food;
KW taste signalling pathway; ds.
XX
XX Homo sapiens.
XX
XX WO200118050-A2.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-US24821.
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XX 10-SEP-1999; 99US-0393634.
XX 22-FEB-2000; 2000US-0510332.
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XX (REGC ) UNIV CALIFORNIA.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Zuker CS, Adler JE, Ryba N, Mueller K, Hoon M;
XX WPI; 2001-211396/21.
XX

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PS Claim 1; SEQ ID NO 14005; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins

CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 15165 BP; 4093 A; 3274 C; 3399 G; 4399 T; 0 other;

Query Match 15.0%; Score 30.8; DB 23; Length 15165;

Best Local Similarity 48.8%; Pred. No. 7.1;

Matches 83; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 24 TACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGA 83

Db 7655 TTCTAATTCTCGGTAATTTACGTTGGCTTACATTTCCGGGTCCCCAAGCCGATATCGAT 7714

QY 84 ACTAAGCAACGGGATACATTTGGGTGGATTGGCAACAACCTTCTGTGACTAACAGGTC 143

Db 7715 ACGAATCGGACAACCTCAATGGTGGTGGTGTGTGCCAGGATTCGTTGATTGAATAGCC 7774

QY 144 CATAGTTTTTCCAGCACACTTCCAGGACGCCATACCGAACAAAGCAAGGT 193

Db 7775 GACATTAGCACACGACATTTCTCGGACTCAAAGTCAAAACAAAGCCATGT 7824

RESULT 7

AAS43104

ID AAS43104 standard; DNA; 325791 BP.

XX

AC AAS43104;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human Oestrogen receptor beta gene.

XX

KW Human; Oestrogen receptor beta; ERbeta; ds; SNP; chromosome 6q.25.1;

KW single nucleotide polymorphism; cardiovascular disease;

KW autoimmune disease; systemic lupus erythematosus; arthritis; rheumatism;

KW osteoarthritis; osteoporosis; breast cancer; endometrial cancer.

XX

OS Homo sapiens.

XX

PN WO200162793-A2.

XX

PD 30-AUG-2001.

XX

PF 20-FEB-2001; 2001WO-US05360.

XX

PR 22-FEB-2000; 2000US-0183755.

PR 24-JAN-2001; 2001US-0768185.

XX

PA (PEKE) PE CORP NY.

XX

PI Kalush F, Cassel MJ, Hwang SS, Winn-Deen ES;

XX

DR WPI; 2001-582041/65.

DR P-PSDB; AAU27322.

XX

XX Oestrogen receptor gene and protein polymorphisms useful for diagnosis

PT of individuals at risk of developing bone disorders -

XX

PS Example 2; Figure 1; 245pp; English.

XX

CC The invention relates to a novel isolated peptide comprising or

CC .consisting of an amino acid sequence selected from an amino acid sequence

CC of a variant oestrogen receptor protein (e.g. ERbeta), or a fragment of

CC 10 amino acids), antibodies against them, nucleic acids encoding

CC them (including vectors for transforming cells). The gene for human

CC ERbeta is located on chromosome 6q.25.1. The variants are encoded

CC by single nucleotide polymorphisms (SNP). The variant peptides and

CC proteins can be used in assays to determine the biological

CC activity of the protein, to raise antibodies, as a reagent in assays

CC designed to quantitatively determine levels of the protein in

CC biological fluids, to identify compounds that modulate receptor

CC activity and to screen compounds for the ability to stimulate or

CC inhibit interaction between the receptor protein and a target molecule

CC that normally interacts with the receptor protein e.g. oestrogen.

CC The antibody can be used to isolate the protein, to assess expression in

CC disease states e.g. cardiovascular disease and autoimmune disease (e.g.

CC systemic lupus erythematosus, arthritis, rheumatism and osteoarthritis),

CC osteoporosis, breast cancer and endometrial cancer. In addition

CC the antibodies can be used in pharmacogenomic analysis and inhibiting

CC protein function, e.g. blocking the binding of the oestrogen receptor

CC protein to a binding partner such as a ligand. The nucleic acids

CC encoding the proteins can be used as probes, primers, chemical

CC intermediates and in biological assays. The present sequence is the

CC human ERbeta gene.

XX

SQ Sequence 325791 BP; 94098 A; 68292 C; 67970 G; 95431 T; 0 other;

Query Match 14.7%; Score 30.2; DB 22; Length 325791;

Best Local Similarity 69.5%; Pred. No. 35;

Matches 41; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 3 TCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTC 61

Db 90917 TGGAGGCATGGTATGGAGGTAATGGTCTTGGCCTCTCTCTCTGATTCAGTCCTTC 90975

RESULT 8

ABQ86047/c

ID ABQ86047 standard; DNA; 335 BP.

XX

AC ABQ86047;

XX

DT 05-SEP-2002 (first entry)

XX

DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 917.

XX

KW Plant; Arabidopsis; transgenic; fungicide; insecticide; ds.

XX

OS Arabidopsis thaliana.

XX

PN US2002062014-A1.

XX

PD 23-MAY-2002.

XX

PF 26-JAN-2001; 2001US-0770791.

XX

PR 27-JAN-2000; 2000US-178480P.

XX

XX (GORL/) GORLACH J.

PA (ANY/) AN Y.

PA (HAMI/) HAMILTON C M.

PA (PRIC/) PRICE J L.

PA (RAIN/) RAINES T M.

PA (YUY/) YU Y.

PA (RAME/) RAMEAKA J G.

PA (PAGE/) PAGE A.

PA (MATH/) MATHAW A V.

PA (LEDF/) LEDFORD B L.

PA (WOES/) WOESSNER J P.

PA (HAAS/) HAAS W D.

PA (GARC/) GARCIA C A.

PA (KRIC/) KRICKER M.

PA (SLAT/) SLATER T.

PA (DAVI/) DAVIS K R.

PA (ALLE/) ALLEN K.

PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX
PI Gurlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Krickler M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
XX WPI; 2002-479265/51.
XX
XX New nucleic acid sequences of Arabidopsis thaliana and their encoded
PT products are useful to produce transgenic plants, to screen for
PT biologically active agents such as fungicides and insecticides and in
PT genetic studies -
XX
XX Claim 1; SEQ ID NO 917; 18pp + Sequence Listing; English.
XX
XX The invention relates to a novel nucleic acid of Arabidopsis thaliana
CC comprising a sequence capable of hybridising under stringency to one of
CC the 999 sequences referred to but not defined in the specification
CC (ABQ85131-ABQ86129). The nucleic acid sequences are useful to identify
CC homologous or related genes, to produce compositions that modulate
CC expression or function of the encoded protein, to map functional regions
CC of the protein, to study associated physiological pathways, to
CC genetically manipulate cells and plants. The encoded products are useful
CC to screen for biologically active agents such as fungicides or
CC insecticides and to elucidate biochemical pathways.
XX
XX Sequence 335 BP; 66 A; 115 C; 51 G; 99 T; 4 other;
SQ
Query Match 14.4%; Score 29.6; DB 24; Length 335;
Best Local Similarity 51.5%; Pred. No. 4.6;
Matches 68; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 15 ATGGACGTATACGAGTTCTTGGTCAATTCCAGGACACAGATGATTCGGTCCAGAACAG 74
Db 262 AAGGAGGGTTATGATTACTGGTTCGATGACCGTTAGATTGCCAATTCGACGGAGAAAG 203
QY 75 GATAATAGAACTAAGCAACGCGATACATAATTGGTGGATTGGCAACAACTTCCTGTGAC 134
Db 202 GATTATTACGGTAGGACCAATGGCTGCGATGGTGGATCGAGAGCGAATGACTGATGAT 143
QY 135 TAACAGGTCCAT 146
Db 142 GCTGAGGACCTT 131
RESULT 9
AAC93962/c
ID AAC93962 standard; cDNA; 498 BP.
XX
AC AAC93962;
XX
XX 19-FEB-2001 (first entry)
XX
DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:457.
XX
XX Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
KW flea infestation; vaccine; antiparasitic; therapeutic target;
KW diagnosis; detection; ss.
XX
OS Ctenocephalides felis.
XX
XX WO2000061621-A2.
PN
XX
PD 19-OCT-2000.
XX
XX 07-APR-2000; 2000WO-US09437.
PF
XX
PR 09-APR-1999; 99US-0128704.
XX
PA (HESK-) HESKA CORP.
XX

PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;
XX
XX WPI; 2000-656323/63.
XX
PT Flea Malpighian tubule and head and nerve cord tissue derived nucleic
PT acids useful for the prevention, diagnosis and treatment of flea
PT infestations -
XX
XX Claim 26; Page 397; 964pp; English.
XX
XX The invention relates to novel cat flea (Ctenocephalides felis) nucleic
CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
CC or head and nerve cord (HNC) tissue. The invention also relates to the
CC encoded proteins. The invention additionally encompasses expression
CC constructs, recombinant viruses and recombinant cells comprising the
CC nucleic acids of the invention, recombinant production of the proteins,
CC antibodies against the proteins, a method of identifying inhibitors of
CC the proteins, and compositions comprising the inhibitors for
CC administration to an animal. The nucleic acids, and the proteins they
CC encode may be used in the prevention, treatment and diagnosis of diseases
CC associated with flea infestations. For example, the nucleic acids may be
CC used to produce an HMT or HNC protein according to standard recombinant
CC DNA methodology by inserting the nucleic acids into a host cell and
CC culturing the cell to express the protein. The HMT and HNC nucleic acids
CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
CC and quantitate the presence of cat flea or other homologous nucleic acid
CC sequences in samples. They may also be used to study the expression and
CC function of the proteins and their role in metabolism. The HMT and HNC
CC proteins may be used as antigens in the production of specific
CC antibodies, and in assays to identify modulators (agonists and
CC antagonists) of HMT and/or HNC protein expression and activity. The
CC anti-HMT/HNC protein antibodies and antagonists may also be used to
CC downregulate protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of flea polypeptides
CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
CC present sequence represents a cat flea HMT cDNA of the invention.
XX
XX Sequence 498 BP; 164 A; 84 C; 88 G; 153 T; 9 other;
SQ
Query Match 14.4%; Score 29.6; DB 21; Length 498;
Best Local Similarity 54.6%; Pred. No. 5.3;
Matches 53; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 39 AATTTCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACGGAT 98
Db 498 AATGTAGCTCAAACTGATAATGCTCACCATGAACAGAAATTATGANCCTTTNATNGGAN 439
QY 99 ACAATTTGGTGGATTGGCAACAACTTCTCTGTGACT 135
Db 438 ACACTGATGTTTNNACGGCTTCAAATCTGGTGTGAAT 402
RESULT 10
ABQ55914
ID ABQ55914 standard; cDNA; 603 BP.
XX
AC ABQ55914;
XX
XX 22-AUG-2002 (first entry)
DT
XX
DE Human ovarian antigen HPCQO91 cDNA, SEQ ID NO:1794.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; gene; ss.
XX

CC compounds useful for the treatment of a disease or condition selected a

CC (f) assessing the prostate cell carcinogenic potential of a compound

CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 526 BP; 164 A; 95 C; 74 G; 193 T; 0 other;

Query Match 14.1%; Score 29; DB 23; Length 526;
Best Local Similarity 54.1%; Pred. No. 8.6;
Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 46 AGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAGCAACGGGATACAATT 105
Db 380 AGGCAAGTGGTGAATAGATCCCAATAAAATAAAGAAATAGATGAATAAGAGATAATA 321

QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCCATAGTTTTTC 154
Db 320 AGACGAATGGAAGACTACATCTTTCTACTGACTGGTCATCGGTTTTTC 272

RESULT 14
AAZ16081
ID AAZ16081 standard; cDNA; 765 BP.
XX
AC AAZ16081;
XX
DT 12-OCT-1999 (first entry)
XX
DE Human gene expression product cDNA sequence SEQ ID NO:3551.
XX
KW Human; gene; gene expression product; diagnosis; therapy; probe;
KW detection; mapping; tissue typing; profiling; forensic; cancer;
KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9938972-A2.
XX
PD 05-AUG-1999.
XX
PF 28-JAN-1999; 99WO-US01619.
XX
PR 03-APR-1998; 98US-0080666.
PR 28-JAN-1998; 98US-0072910.
PR 24-FEB-1998; 98US-0075954.
PR 31-MAR-1998; 98US-0080114.
PR 03-APR-1998; 98US-0080515.
XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
PI Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
PI Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
PI Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
PI Stache-Crain B, Sudduth-Klinger J, Williams LT;
XX
DR WPI; 1999-494092/41.
XX
PT Novel human genes and their expression products which are
PT differentially expressed in different cell types
XX
PS Claim 1; Page 1695; 2479pp; English.
XX
CC The present invention describes a library of human polynucleotides
CC comprising the sequences given in AAZ12532 to AAZ1779. Also described is
CC a method of detecting differentially expressed genes correlated with the
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample from a cell
CC suspected of being cancerous, where the gene product is encoded by one
CC of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The
CC polynucleotides can be used as a source of primers and probes, which can
CC be used for a variety of purpose, e.g. detection of expression levels,

CC mapping, tissue typing or profiling, forensics, genetic analysis and
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC can be used for raising antibodies for experimental, diagnostic and
CC therapeutic purposes. The polynucleotides may also be used to construct
CC arrays for diagnostics (which may be used to determine function of an
CC encoded protein); and to detect differences in expression levels between
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC identify a genetic predisposition or susceptibility to a disease such as
CC cancer). The polynucleotides of the invention are especially used in the
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC and lung cancer. The polynucleotides can also be used to screen for
CC peptide analogues and antagonists.
XX
SQ Sequence 765 BP; 204 A; 145 C; 186 G; 227 T; 3 other;

Query Match 14.1%; Score 29; DB 20; Length 765;
Best Local Similarity 54.9%; Pred. No. 9.8;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 31 TCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAGC 90
Db 17 TCTTGTCTCTNTTTCAGGATCCCATCGATTCCGAAAGAGATGGTTCAGGAGGAAAGC 76

QY 91 AACGGGATACAAATTTGGTGGATTGGCAACAACTTCCTGTG 132
Db 77 CAAGATGGAAATGGATGGGAATGAATGAGGAACATGATGTG 118

RESULT 15
AAT47073/c
ID AAT47073 standard; RNA; 8543 BP.
XX
AC AAT47073;
XX
DT 15-APR-1997 (first entry)
XX
DE Maize dwarf mosaic virus genomic RNA.
XX
KW MDMV-B; viral resistance; disease resistance; transgenic plant;
KW monocot; P3 proteinase; N1a proteinase; N1b replicase;
KW RNA-dependent RNA polymerase; coat protein; Zea mays; sorghum;
KW sugarcane; Saccharum officinale; ss.
XX
OS Maize dwarf mosaic virus strain B.
XX
FH Key Location/Qualifiers
FT CDS 3..8291
FT /*tag= a
FT /product= polyprotein encoded by MDMV-B genome
FT 3'UTR 8292..8530
FT /*tag= b
FT misc_RNA 3..1133
FT /*tag= c
FT /product= 3-prime sequence of helper component
FT misc_RNA 1134..2375
FT /*tag= d
FT /product= P3 proteinase
FT misc_RNA 2376..4292
FT /*tag= e
FT /product= cylindrical inclusion protein
FT misc_RNA 4293..4451
FT /*tag= f
FT /product= K2 (6 kDa protein)
FT misc_RNA 4452..5744
FT /*tag= g
FT /product= N1a proteinase
FT misc_RNA 5745..7307
FT /*tag= h
FT /product= N1b replicase
FT misc_RNA 7308..8291
FT /*tag= i
FT /product= coat protein

XX WO9702352-A1.
PN
XX
XX
PD
XX
XX
XX
PF 20-JUN-1996; 96WO-EP02673.
XX
XX
PR 30-JUN-1995; 95US-0496944.
XX
XX
PA (CIBA) CIBA GEIGY AG.
XX
XX Dietz JM, Law MD;
PI
XX
XX
DR WPI; 1997-108965/10.
DR P-PSDB; AAW10344.
XX
XX
PT Chimaeric gene for imparting viral resistance to plants - contains
PT sequence modified to express non-translatable mRNA, or non-coat
PT viral protein
XX
XX
PS Disclosure; Page 31-44; 64pp; English.
XX
XX
CC The sequence of the polycistronic messenger RNA of maize dwarf
CC mosaic virus strain B (MDMV-B) is given in AAT47073 and the encoded
CC MDMV-B polyprotein in AAW10344. New chimaeric genes (see also
CC AAT47074) comprise a monocotyledonous plant promoter linked to a
CC modified nucleic acid sequence derived from the MDMV-B genome. The
CC modification is such that mRNA is translated to a truncated protein
CC (pref. smaller than 200 amino acids), no translation of mRNA occurs
CC or the transcribed mRNA lacks the translation initiation codon or
CC includes a premature stop codon. Expression of the chimaeric gene
CC inhibits infection of plants (pref. sorghum, sugarcane, esp. maize)
CC by MDMV. The transgenic plants display an inheritable resistance
CC trait.
XX
SQ Sequence 8543 BP; 2913 A; 1637 C; 1820 G; 2160 U; 13 other;
Query Match 14.1%; Score 29; DB 18; Length 8543;
Best Local Similarity 52.0%; Pred. No. 24;
Matches 65; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 14 TATGGACGTATACGAGTTCTTGGTCAATTTCAGGACACAGATGATTCGGTCCAGAAC 73
Db
1679 TCTGAACACACGCCATATTGCTGAATAATTTCCACAGTATGCAATTTGCCCCATGATTG 1620
QY 74 GGATAATAGAACTAAGCAACCGCATACAATTTGGTGGATTGGCAACAACTTCCTGTGA 133
Db
1619 GTTTAATTGATCTACGTAACTTTTTCATCAGGGTGTATAGGCGCTCGTCATATAGTGC 1560
QY 134 CTAAC 138
Db 1559 ATACC 1555
RESULT 16
AAK95240
ID AAK95240 standard; DNA; 1503900 BP.
XX
AC AAK95240;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human neuregulin-1 gene.
XX
KW Human; neuregulin-1 associated gene 1; NRG1AG1; Schizophrenia gene;
KW gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200164876-A2.
XX
PD 07-SEP-2001.
XX

PF 28-FEB-2001; 2001WO-US06376.
XX
PR 28-FEB-2000; 2000US-0515715.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Stefansson H, Steinthorsdottir V, Gulcher JR;
XX
DR WPI; 2001-550179/61.
DR P-PSDB; AAG67900, AAG67901, AAG67902, AAG67903, AAG67904, AAG67905,
DR AAG67906, AAG67907, AAG67908, AAG67909, AAG67910, AAG67911, AAG67912,
DR AAG67913, AAG67914, AAG67915, AAG67916, AAG67917, AAG67918, AAG67919,
DR AAG67920, AAG67921, AAG67922, AAG67923, AAG67924, AAG67925, AAG67926,
DR AAG67927, AAG67928, AAG67929, AAG67930, AAG67931, AAG67932, AAG67933,
DR AAG67934, AAG67935, AAG67936, AAG67937.
XX
PT Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for
PT preventing diagnosing and treating schizophrenia -
XX
XX
PS Disclosure; Page 90-501; 750pp; English.
XX
XX
CC This sequence represents the human neuregulin-1 associated gene 1
CC (NRG1AG1) of the invention. The NRG1AG1 gene is also referred to as the
CC human Schizophrenia gene. The invention also relates to fragments or
CC variants of the gene and the NRG1AG1 polypeptides they encode. The
CC NRG1AG1 nucleic acids and polypeptides may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate NRG1AG1
CC expression. For example, they may be used to treat disorders associated
CC with decreased expression by rectifying mutations or deletions in a
CC patient's genome that affect the activity of NRG1AG1 by expressing
CC inactive proteins or to supplement the patients own production of
CC NRG1AG1. Additionally, the gene may be used to produce NRG1AG1
CC polypeptides, by inserting the nucleic acids into a host cell and
CC culturing the cell to express the protein. The gene may also be used as
CC DNA probes and primers in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acids in samples, and therefore which
CC patients may be in need of restorative therapy. The NRG1AG1 polypeptides
CC may also be used as antigens in the production of antibodies against
CC NRG1AG1 and in assays to identify modulators of NRG1AG1 expression and
CC activity. Anti-NRG1AG1 antibodies and antagonists may also be used to
CC down regulate expression and activity. Anti-NRG1AG1 antibodies may
CC also be used as diagnostic agents for detecting the presence of NRG1AG1
CC polypeptides in samples. NRG1AG1 is associated with schizophrenia which
CC may be prevented, diagnosed and/or treated by the above methods.
XX
SQ Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
Query Match 14.1%; Score 29; DB 22; Length 1503900;
Best Local Similarity 54.1%; Pred. No. 1.5e+02;
Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 46 AGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAAGCAACGCGATACAATT 105
Db 504749 AGGCAAGTGGTGAATAGATCCCAATAAAATAAAGAAATAGATGAATAAGAGATAATA 504808
QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTC 154
Db 504809 AGACGAATGGAGACTACATTCTTCTTCTACTGACTGGTCATCGGTTTTC 504857
RESULT 17
AAK96733
ID AAK96733 standard; DNA; 1503900 BP.
XX
AC AAK96733;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human neuregulin-1 gene.
XX
KW Human; neuregulin 1 gene; schizophrenia; gene therapy; ds.
XX
OS Homo sapiens.

XX WO200164877-A2.
PN
XX 07-SEP-2001.
PD
XX 28-FEB-2001; 2001WO-US06377.
PF
XX
XX 28-FEB-2000; 2000US-0515716.
PR
XX (DECO-) DECODE GENETICS EHF.
PA
XX
PI Stefansson H, Steinhorsdottir V, Gulcher JR;
XX
XX WPI; 2001-514841/56.
DR P-PSDB; AAG67938, AAG67939, AAG67940, AAG67941, AAG67942, AAG67943,
DR AAG67944, AAG67945, AAG67946, AAG67947, AAG67948, AAG67949,
DR AAG67950, AAG67951, AAG67952, AAG67953, AAG67954, AAG67955,
DR AAG67956, AAG67957, AAG67958, AAG67959, AAG67960, AAG67961,
DR AAG67962, AAG67963, AAG67964, AAG67965, AAG67966, AAG67967,
DR AAG67968, AAG67969, AAG67970, AAG67971, AAG67972, AAG67973,
DR AAG67974, AAG67975.
XX
PT Neuregulin 1 nucleic acids and proteins useful for diagnosing
PT preventing and treating schizophrenia -
XX
PS Disclosure; Page 345-756; 756pp; English.
XX
CC This sequence represents the human neuregulin 1 gene of the invention.
CC The invention also relates to fragments or variants of the neuregulin 1
CC gene. The gene and its proteins may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate neuregulin 1
CC expression, such as schizophrenia. For example they may be used to treat
CC disorders associated with decreased neuregulin 1 expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC neuregulin 1 by expressing inactive proteins or to supplement the
CC patients own production of polypeptides. Additionally, the gene may be
CC used to produce the neuregulin 1 protein, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The gene
CC and its complementary sequences may also be used as DNA probes in
CC diagnostic assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. The protein may also be used as antigens in the
CC production of antibodies against neuregulin 1 and in assays to identify
CC modulators of neuregulin 1 expression and activity. The antibodies and
CC antagonists may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of neuregulin 1 in samples.
XX
SQ Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
Query Match 14.1%; Score 29; DB 22; Length 1503900;
Best Local Similarity 54.1%; Pred. No. 1.5e+02;
Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 46 AGGACACAGATGATTCGGTCCAAAGAACAGGATATAGAACTAAGCAACGCGATACAATTT 105
Db 504749 AGGCAAGTGGTGAATAGATCCCAATAAAAAATAAGAAATAGATGAATAAGAAATATA 504808
QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGTCCATAGTTTTC 154
Db 504809 AGACGAATGGAAGACTACATCTTTCTACTGACTGCTCATCGGTTTTC 504857
RESULT 18
AAFI11182
ID AAFI11182 standard; cDNA; 300 BP.
XX
AC AAFI11182;
XX
DT 13-MAR-2001 (first entry)
XX
DE Fusarium venenatum EST SEQ ID NO:3705.
XX

KW Multiple gene expression; filamentous fungal cell; EST;
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS Fusarium venenatum.
XX WO2000056762-A2.
PN
XX
XX 28-SEP-2000.
PD
XX
XX 22-MAR-2000; 2000WO-US07781.
PF
XX
XX 22-MAR-1999; 99US-0273623.
PR
XX (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
XX
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX WPI; 2000-594572/56.
DR
XX
XX Monitoring differential expression of genes in filamentous fungal cells
PT uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags -
XX
XX Claim 86; Page 1672; 3161pp; English.
PS
XX The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the
CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway
CC engineering. Using ESTs provides several advantages over genomic or
CC random cDNA clones including elimination of redundancy as one spot on an
CC array equals one gene or open reading frame, and organisation of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC all specifically claimed in the present invention.
XX
SQ Sequence 300 BP; 86 A; 53 C; 65 G; 90 T; 6 other;

Query Match 14.0%; Score 28.8; DB 21; Length 300;
Best Local Similarity 50.8%; Pred. No. 8.2;
Matches 66; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 70 AACAGGATAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAACTTCCT 129
Db 139 ATCTTGTGTTTATGATGACNAATTGTCATTGATATTTGGCGGATTGGCAACTTGCTATAT 198
QY 130 GTGACTAACAGGTCCATAGTTTTTTCACGACACTTCCAGGACGCCATACCGAACAAGCA 189
Db 199 TTTACCTGCTGCTTCANAGACACCCCGCGGCGACTAGAACACATACACAGACAACACACA 258
QY 190 AGGTGTTATT 199
Db 259 AGCTGTTCTT 268

RESULT 19
AAV52349
ID AAV52349 standard; DNA; 2651 BP.
XX
AC AAV52349;
XX
DT 23-OCT-1998 (first entry)
XX
DE Streptococcus pneumoniae genome fragment SEQ ID NO:216.
XX
KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
KW computer readable medium; vaccine; pharmaceutical composition; ds.
XX
OS Streptococcus pneumoniae.
XX
PN WO9818931-A2.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US19588.
XX
PR 31-OCT-1996; 96US-0029960.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
PI Kunsch CA, Rosen CA;
XX
DR WPI; 1998-272225/24.
XX
PT Computer-readable medium with recorded Streptococcus pneumoniae
PT polynucleotide sequences - useful in diagnostic kits and assays, and
PT pharmaceutical compositions and vaccines for Streptococcus
PT pneumoniae
XX
PS Claim 1; Page 1220-1222; 1409pp; English.
XX
CC The present invention describes a computer readable medium which has
CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)
CC recorded on it, or a representative fragment or a sequence at least 95%
CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in
CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
CC Streptococcus pneumoniae. The present invention also describes an
CC isolated nucleic acid molecule encoding a homologue of any of the
CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the
CC nucleic acid molecule is produced by a process comprising: (a) screening
CC a genomic DNA library using as a probe a target sequence defined by any
CC of the sequences in SEQ ID NO:1 to 391, identifying members of the
CC library which contain sequences that hybridize to the target sequence and
CC isolating the nucleic acid molecules from the members; or (b) isolating
CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid
CC molecules whose nucleotide sequence is homologous to amplification
CC primers derived from the fragment of the S. pneumoniae genome to prime
CC the amplification and isolating the amplified sequences. The computer
CC readable medium can be used in a computer-based system for identifying
CC fragments of the S. pneumoniae genome of commercial importance, or
CC expression modulating fragments of the S. pneumoniae genome. Products
CC from the present invention can be used in diagnosis kits and assays, and
CC pharmaceutical compositions and vaccines for S. pneumoniae.
XX
SQ Sequence 2651 BP; 874 A; 505 C; 456 G; 815 T; 1 other;

Query Match 14.0%; Score 28.8; DB 19; Length 2651;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 45; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 99 ACAATTTGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCATAGTTTTCACGA 158
DB 2357 ACCAAAGGATTGTTGATAAGCTACTTCTGTCTCTAACAATTCCTAGCTTGATCCGA 2416

QY 159 CACTTCCAAGGA 170
DB 2417 CTCTAAGAAGGA 2428

RESULT 20
ABL21466
ID ABL21466 standard; DNA; 4718 BP.
XX
AC ABL21466;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15871.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 15871; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4718 BP; 1467 A; 1018 C; 892 G; 1341 T; 0 other;

Query Match 14.0%; Score 28.8; DB 23; Length 4718;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 45 CAGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAAGCAACGCGATACAATT 104
DB 3466 CAGCACAAATGATGTTTATGACTGATTAAGAAATAGAACCAACAAACGTTTACGTTA 3525

QY 105 TGGTGGATTGGCAACAAAC 124
DB 3526 AGGTGTTCTCTGAAATAAAC 3545

RESULT 21
ABL30302/c
ID ABL30302 standard; DNA; 23732 BP.
XX
AC ABL30302;
XX
DT 26-MAR-2002 (first entry)
XX

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42379.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 42379; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 23732 BP; 6358 A; 4988 C; 5137 G; 7249 T; 0 other;

Query Match 14.0%; Score 28.8; DB 23; Length 23732;
Best Local Similarity 52.5%; Pred. No. 40;
Matches 63; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 6 ACCCATGGTATGGACGATATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
Db 19442 ACCCATAGATCACCGATCTCAGATCTCTTGGTTATTATAGAGCTGCTGAAACGTCAGTG 19383

QY 66 CAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAACT 125
Db 19382 AAAGGAAAAGATGTTTCGTATACGCAACGCGATTTCGATTAGAGTGCCATAAAATAACT 19323

RESULT 22
AAF94886
ID AAF94886 standard; cDNA; 396 BP.
XX
AC AAF94886;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human ovarian cancer associated coding sequence SEQ ID NO: 77.
XX
KW Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200118046-A2.
XX
PD 15-MAR-2001.
XX

PF 08-SEP-2000; 2000WO-US24827.
XX
PR 10-SEP-1999; 99US-0394374.
PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA;
XX
DR WPI; 2001-211395/21.
XX
XX Isolated polypeptides associated with ovarian carcinomas, and the
PT nucleic acids that encode them, useful for the prevention diagnosis and
PT treatment of ovarian cancers -
XX
PS Claim 18; Page 140; 189pp; English.
XX
CC The present invention provides a number of coding sequences and proteins,
CC the over-expression of which is associated with ovarian carcinoma/cancer.
CC These can be used in the diagnosis, treatment and prevention of ovarian
CC cancer, optionally by gene therapy or in the form of a vaccine. The
CC present sequence is an example of one of these sequences.
XX
SQ Sequence 396 BP; 123 A; 64 C; 53 G; 136 T; 20 other;

Query Match 13.9%; Score 28.6; DB 22; Length 396;
Best Local Similarity 50.4%; Pred. No. 11;
Matches 58; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 36 GTCAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAAGCAACGC 95
Db 74 GTTAAATNCNGGACNCCTTACAATTGTGTAAANAACATGCNCANAAACATATGCATATA 133

QY 96 GATACAATTTGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCATAGTT 150
Db 134 ACTACTATACAGGNGATNTGCAAAAACCCCTACTGGGAAATCCATTTCATTAGTT 188

RESULT 23
ABT03153
ID ABT03153 standard; cDNA; 396 BP.
XX
AC ABT03153;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 77.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
PR 03-APR-2001; 2001US-0825294.
PR 02-OCT-2001; 2001US-0970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX
DR WPI; 2002-500186/53.
XX
PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in

PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PT -

XX Example 1; Page 139; 197pp; English.

XX The present invention provides human ovarian cancer associated proteins and coding sequences. The sequences can be used in the diagnosis and treatment of ovarian cancers. The present sequence is a coding sequence of the invention.

SQ Sequence 396 BP; 123 A; 64 C; 53 G; 136 T; 20 other;

Query Match 13.9%; Score 28.6; DB 24; Length 396;

Best Local Similarity 50.4%; Pred. No. 11;

Matches 58; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 36 GTCAATTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAGCAACGC 95

Db 74 GTTAAATNCNGGGACNCCTTACAATTGTGTAAANAACATGCNCANAAACATATGCATATA 133

QY 96 GATACAAATTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTT 150

Db 134 ACTACTATACAGGNGATNTGCAAAACCCCTACTGGGAAATCCATTTTCATTAGTT 188

RESULT 24

ABL48836

ID ABL48836 standard; cDNA; 396 BP.

XX

AC ABL48836;

XX

DT 18-JUN-2002 (first entry)

XX

DE Ovarian carcinoma sequence isolate 24679.

XX

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

KW ss.

XX

OS Homo sapiens.

XX

PN US2002004491-A1.

XX

PD 10-JAN-2002.

XX

PF 03-APR-2001; 2001US-0825294.

XX

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.

XX

PA (XUJJ/) XU J.

PA (STOL/) STOLK J A.

PA (ALGA/) ALGATE P A.

PA (FLIN/) FLING S P.

XX

PI Xu J, Stolk JA, Algate PA, Fling SP;

XX

DR WPI; 2002-171027/22.

XX

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis, prevention and/or treatment of cancer, especially ovarian cancer -

XX

PS Example 1; Page 64; 131pp; English.

XX

CC The invention relates to ovarian tumour polynucleotides and polypeptides that may be utilised in cancer therapy, for example in a vaccine or gene therapy. Polypeptides and polynucleotides of the invention are useful for detecting a cancer in a patient, for stimulating and/or expanding T-cells specific for a tumour protein, and for inhibiting the development of a cancer in a patient. They are also useful for stimulating an immune response in a patient, and for treating a cancer in

CC a patient and for determining the presence of a cancer in a patient.

CC The isolated polynucleotides of the invention are useful for their ability to selectively form duplex molecules with complementary stretches of the entire desired gene or gene fragments, and for designing and preparing ribozyme molecules for inhibiting expression of tumour polypeptides in tumour cells. Polypeptides and polynucleotides of the invention are also useful in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. The sequences given in records ABL48760-ABL48956 represent polynucleotides encoding ovarian carcinoma proteins.

XX

SQ Sequence 396 BP; 123 A; 64 C; 53 G; 136 T; 20 other;

Query Match 13.9%; Score 28.6; DB 24; Length 396;

Best Local Similarity 50.4%; Pred. No. 11;

Matches 58; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 36 GTCAATTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAGCAACGC 95

Db 74 GTTAAATNCNGGGACNCCTTACAATTGTGTAAANAACATGCNCANAAACATATGCATATA 133

QY 96 GATACAAATTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTT 150

Db 134 ACTACTATACAGGNGATNTGCAAAACCCCTACTGGGAAATCCATTTTCATTAGTT 188

RESULT 25

AAV17601/c

ID AAV17601 standard; DNA; 1825 BP.

XX

AC AAV17601;

XX

DT 20-JUL-1998 (first entry)

XX

DE Yeast AFC1 gene encoding Afc1p protein.

XX

KW AFC1 gene; Afc1p; a-factor convertase; CAAX protease;

KW zinc metalloprotease; yeast; prenylation; Ras; inhibitor; cancer;

KW colorectal carcinoma; pancreas carcinoma; leukaemia; therapy; ss.

XX

OS Saccharomyces cerevisiae.

XX

FH Location/Qualifiers

FT CDS 342..1704

FT /*tag= a

FT /transl_except= (pos:378..380, aa:Thr)

FT /transl_except= (pos:702..705, aa:Ser)

FT /note= "this codon has an apparent 1 nucleotide insertion, which alters the reading frame"

FT /transl_except= (pos:1255..1257, aa:Met)

FT /transl_except= (pos:1663..1665, aa:Leu)

XX

PN WO9805786-A2.

XX

PD 12-FEB-1998.

XX

PF 06-AUG-1997; 97WO-US14777.

XX

PR 30-JUL-1997; 97US-0902774.

PR 07-AUG-1996; 96US-0023491.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Ashby MN, Boyartchuk VL, Rine JD;

XX

DR WPI; 1998-145621/13.

DR P-PSDB; AAW48301.

XX

PT Vector comprising nucleic acid coding for Afc1p and Rcelp proteins involved in protein prenylation - useful for screening for inhibitors of proteins, especially of mutated ras proteins involved in cancerous conditions

PT

PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.
Query Match 13.9%; Score 28.6; DB 21; Length 1920;		
Best Local Similarity 57.1%; Pred. No. 19;		
Matches 52; Conservative 0; Mismatches 39; Indels 0; Gaps 0;		
QY	19	ACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATA 78
Db	236	ATGGATACGTTAACTTCACCAATCCCAAGACGCTGCAAGAGCGATCCAAGAACTGAATT 295
QY	79	ATAGAACTAAGCAACGCGATACAAATTGGGT 109
Db	296	ACATACCTCTTTATGGAAAACCTATTAGGGT 326
RESULT 27		
AAC45029		
ID	AAC45029 standard; DNA; 2090 BP.	
XX		
AC	AAC45029;	
XX		
DT	18-OCT-2000 (first entry)	
XX		
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 45033.	
XX		
KW	Hybridisation assay; genetic mapping; gene expression control;	
KW	protein identification; signal transduction pathway;	
KW	metabolic pathway; promoter; termination sequence; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-0301439.	
XX		
PR	25-FEB-1999;	99US-0121825.
PR	05-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131449.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.


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CC flora of human upper airways. M. catarrhalis is known to cause acute,
CC localised infections such as otitis media, sinusitis and bronchopulmonary
CC infection and life-threatening, systemic diseases including endocarditis
CC and meningitis.
CC
XX
SQ Sequence 66986 BP; 18889 A; 13427 C; 15112 G; 19558 T; 0 other;
Query Match 13.9%; Score 28.6; DB 22; Length 66986;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 55; Conservative 0; Mismatches 44; Indels 0; Gaps 0
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2922 TTGGTGGCTTCGGCAAAACTTGCTTTAAATGACAAGCAGGTGAGATGACACAAGACATG 2981
QY 165 CAAGGACGCCATACCGAACAAAGCAAGGTGTTATTATCC 203
Db || || || || || || || || || || || || || || || || || || || || ||
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RESULT 29
ABN71527
ID ABN71527 standard; DNA; 2155561 BP.
XX
AC ABN71527;
XX
DT 02-JUL-2002 (first entry)
XX
DE Streptococcus polynucleotide SEQ ID NO 10967.
XX
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX
OS Streptococcus sp.
XX
PN WO200234771-A2.
XX
XX 02-MAY-2002.
XX
XX 29-OCT-2001; 2001WO-GB04789.
XX
XX 27-OCT-2000; 2000GB-0026333.
XX
XX 24-NOV-2000; 2000GB-0028727.
XX
XX 07-MAR-2001; 2001GB-0005640.
XX
XX (CHIR-) CHIRON SPA.
XX
XX (GENO-) INST GENOMIC RES.
XX
PI Telford J, Massignani V, Margarit Ros VI, Grandi G, Fraser C;
PI Tettelin H;
XX
XX WPI; 2002-352536/38.
XX
XX New Streptococcus protein for the treatment or prevention of infection
XX or disease caused by Streptococcus bacteria, such as meningitis, and
XX for detecting a compound that binds to the protein -
XX
XX Claim 8; Page 4196-4488; 4525pp; English.
XX
XX The invention relates to a protein (ABP25413-ABP30895) from group B
XX streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
XX the specification. The proteins have antibacterial and antiinflammatory
XX activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
XX antibodies that bind (I) are used in the manufacture of medicaments for
XX the treatment or prevention of infection or disease caused by
XX Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
XX Nucleic acids encoding (I) are used to detect Streptococcus in a
XX biological sample. (I) is used to determine whether a compound binds to
XX (I). A composition comprising (I) or a nucleic acid encoding (I), may be
XX used as a vaccine or diagnostic composition. The disease caused by
XX Streptococcus that is prevented or treated may be meningitis. Nucleic

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PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-451929/48.
DR
XX
PT Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the reproductive system including prostate cancer
PT and also for testing and detection e.g. diagnosis -
XX
PS Disclosure; SEQ ID No 819; 546pp; English.
XX

CC The invention relates to novel isolated human prostate cancer antigen
CC polynucleotides (I) and polypeptides (II). (I) and (II) are useful for
CC preventing, treating or ameliorating a medical condition when
CC administered. (I), (II) and the antibody to (II) are useful for treating,
CC preventing and/ or prognosing disorders related to the reproductive
CC system including prostate cancers; urinary disorders e.g. chronic
CC nephritis; and blood-related disorders e.g. thrombosis. (II) can be used
CC for testing and detection e.g. as a chromosomal marker and in forensics.
CC (I) and the anti-(II) antibody can be used in testing and detection in
CC immunoassays. AAS40061-AAS40775 represent the human prostate cancer
CC antigen coding sequences, and related PCR primers and sequences of the
CC invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
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SQ Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;

Query Match 13.8%; Score 28.4; DB 22; Length 415;
Best Local Similarity 54.9%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 25 ACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGACAGGATAATAGAA 84
DB 343 ACCACTGGTTTATGATAATCTAGGTGCCAGATGATGGTGTCTTAGGTACGGGTGATGCA 284

QY 85 CTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAACTT 126
DB 283 GTGAAGAAACAGTAAAGTGAATGGATTCTGGATATATTT 242

RESULT 31
AAS40668/c
ID AAS40668 standard; DNA; 415 BP.

XX AAS40668;

XX 17-DEC-2001 (first entry)

XX DNA encoding human prostate cancer antigen, Seq ID No 820.

KW Human; prostate cancer antigen; cytostatic; uropathic; diagnostic;
KW reproductive system; chromosomal marker; forensic; urinary disorder;
KW chronic nephritis; blood-related disorder; thrombosis; ds.

OS Homo sapiens.

XX WO200155316-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01328.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

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XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

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XX 07-JUL-2000; 2000US-0216880.

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XX 14-AUG-2000; 2000US-0225447.

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11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;
WPI; 2001-451929/48.

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancer and also for testing and detection e.g. diagnosis -

Disclosure; SEQ ID No 820; 546pp; English.

The invention relates to novel isolated human prostate cancer antigen polynucleotides (I) and polypeptides (II). (I) and (II) are useful for preventing, treating or ameliorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancers; urinary disorders e.g. chronic nephritis; and blood-related disorders e.g. thrombosis. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in immunoassays. AAS40061-AAS40775 represent the human prostate cancer antigen coding sequences, and related PCR primers and sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.

Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;

Query Match	13.8%	Score 28.4;	DB 22;	Length 415;
Best Local Similarity	54.9%	Pred. No. 13;		
Matches 56;	Conservative 0;	Mismatches 46;	Indels 0	

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RESULT 32
AAS40669/c
ID AAS40669 standard; DNA; 415 BP.

AC AAS40669;

DT 17-DEC-2001 (first entry)

DE DNA encoding human prostate cancer antigen, Seq ID No 821.

Human; prostate cancer antigen; cytostatic; uropathic; diagnostic; reproductive system; chromosomal marker; forensic; urinary disorder; KW

PR, 17-NOV-2000; 2000US-0249245.

chronic nephritis; blood-related disorder; thrombosis; ds.

KW	PR	25-SEP-2000;	2000US-0234998.
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OS	PR	27-SEP-2000;	2000US-0235834.
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PR	PR	02-OCT-2000;	2000US-0237040.
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PR	PR	13-OCT-2000;	2000US-0239937.
PR	PR	20-OCT-2000;	2000US-0240960.
PR	PR	20-OCT-2000;	2000US-0241221.
PR	PR	20-OCT-2000;	2000US-0241785.
PR	PR	20-OCT-2000;	2000US-0241786.
PR	PR	20-OCT-2000;	2000US-0241787.
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PR	PR	08-NOV-2000;	2000US-0246532.
PR	PR	08-NOV-2000;	2000US-0246609.
PR	PR	08-NOV-2000;	2000US-0246610.
PR	PR	08-NOV-2000;	2000US-0246611.
PR	PR	08-NOV-2000;	2000US-0246613.
PR	PR	17-NOV-2000;	2000US-0249207.
PR	PR	17-NOV-2000;	2000US-0249208.
PR	PR	17-NOV-2000;	2000US-0249209.
PR	PR	17-NOV-2000;	2000US-0249210.
PR	PR	17-NOV-2000;	2000US-0249211.
PR	PR	17-NOV-2000;	2000US-0249212.
PR	PR	17-NOV-2000;	2000US-0249213.
PR	PR	17-NOV-2000;	2000US-0249214.
PR	PR	17-NOV-2000;	2000US-0249215.
PR	PR	17-NOV-2000;	2000US-0249216.
PR	PR	17-NOV-2000;	2000US-0249217.
PR	PR	17-NOV-2000;	2000US-0249218.
PR	PR	17-NOV-2000;	2000US-0249244.
PR	PR	17-NOV-2000;	2000US-0249245.
PR	PR	17-NOV-2000;	2000US-0249264.
PR	PR	17-NOV-2000;	2000US-0249265.
PR	PR	17-NOV-2000;	2000US-0249297.
PR	PR	17-NOV-2000;	2000US-0249299.
PR	PR	17-NOV-2000;	2000US-0249300.
PR	PR	01-DEC-2000;	2000US-0250160.
PR	PR	01-DEC-2000;	2000US-0250391.
PR	PR	05-DEC-2000;	2000US-0251030.
PR	PR	05-DEC-2000;	2000US-0251988.
PR	PR	05-DEC-2000;	2000US-0256719.
PR	PR	06-DEC-2000;	2000US-0251479.
PR	PR	08-DEC-2000;	2000US-0251856.
PR	PR	08-DEC-2000;	2000US-0251868.
PR	PR	08-DEC-2000;	2000US-0251869.
PR	PR	08-DEC-2000;	2000US-0251989.
PR	PR	08-DEC-2000;	2000US-0251990.
PR	PR	11-DEC-2000;	2000US-0254097.
PR	PR	05-JAN-2001;	2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-451929/48.
XX Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the reproductive system including prostate cancer
PT and also for testing and detection e.g. diagnosis -
XX Disclosure; SEQ ID No 821; 546pp; English.
PS The invention relates to novel isolated human prostate cancer antigen
XX polynucleotides (I) and polypeptides (II). (I) and (II) are useful for
CC preventing, treating or ameliorating a medical condition when
CC administered. (I), (II) and the antibody to (II) are useful for treating,
CC preventing and/ or prognosing disorders related to the reproductive
CC system including prostate cancers; urinary disorders e.g. chronic
CC nephritis; and blood-related disorders e.g. thrombosis. (II) can be used
CC for testing and detection e.g. as a chromosomal marker and in forensics.
CC (I) and the anti-(II) antibody can be used in testing and detection in
CC immunoassays. AAS40061-AAS40775 represent the human prostate cancer
CC antigen coding sequences, and related PCR primers and sequences of the
CC invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;

Query Match 13.8%; Score 28.4; DB 22; Length 415;
Best Local Similarity 54.9%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 25 ACGAGTTCTTGGTCAATTCAGGACACAGATCGGTCCTCAAGAACAGGATAATAGAA 84
Db 343 ACCACTGGTTTATGATAATCTAGGTGCCAGATGATGGTCTTAGGTCAGGGTGATAGCA 284

QY 85 CTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAACTT 126
Db 283 GTGGAAGAAACAGTAAAAAGTGATTGGATTCTGGATATATTT 242

RESULT 33
AAL06555/C
ID AAL06555 standard; DNA; 415 BP.
XX AAL06555;
AC AAL06555;
XX 21-NOV-2001 (first entry)
DT Human reproductive system related antigen DNA SEQ ID NO: 9243.
XX Human reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX Homo sapiens.
OS WO200155320-A2.
XX 02-AUG-2001.
PD 17-JAN-2001; 2001WO-US01339.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.

PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.

PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-465570/50.

XX Isolated nucleic acid molecule encoding a reproductive system antigen

PT is used in preventing, treating or ameliorating a medical condition -

XX

PS Disclosure; SEQ ID NO 9245; 1297pp + Sequence Listing; English.

XX

CC The present invention provides the protein and coding sequences of a

CC number of human reproductive system related antigens. These can be used

CC in the prevention and treatment of reproductive system disorders,

CC including cancer. The present sequence is a genomic sequence encoding a

CC protein of the invention.

XX

SQ Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;

Query Match 13.8%; Score 28.4; DB 22; Length 415;

Best Local Similarity 54.9%; Pred. No. 13;

Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 25 ACGAGTTCTTGGTCAATTTCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAA 84

Db 343 ACCACTGGTTTATGATAATCTAGGTGCCAGATGATGGTGCTTAGGTCAGGGTGATAGCA 284

QY 85 CTAAGCAACGCGATACAAATTGGTGGATTGGCAACAAACTT 126

Db 283 GTGGAAGAAACAGTAAAGTGATTGGATTCTGGATATATTT 242

RESULT 36

AAQ15229/c

ID AAQ15229 standard; DNA; 1796 BP.

XX

AC AAQ15229;

XX

DT 11-MAR-1992 (first entry)

XX

DE BBRP42 gene.

XX

XX Signal peptide; promoter; transcription control; protease;

KW IFN; IL; EGF; GM-CSF; Factor VIII; insulin; TNF; NGF;

KW vector; foreign protein; ss.

XX

OS Bacillus brevis.

XX

FH Key Location/Qualifiers

FT CDS 237..1607

FT /*tag= a

FT /label= BBRP42

FT sig_peptide 237..320

FT /*tag= b

FT promoter 115..184

FT /*tag= c

FT note= "claim 5, page 29"

FT misc_signal 186..236

FT /*tag= a

FT /label= transcription control_region

FT note= "claim 6, page 29"

XX

PN WO9118101-A.

XX

XX 28-NOV-1991.

PD

XX

PF 10-MAR-1991; 91WO-JP00626.

XX

PR 30-NOV-1990; 90JP-0334575.

PR 11-MAY-1990; 90JP-0122166.

XX

XX (FARH) HOECHST JAPAN LTD.

PA

XX Hashimoto T, Tsujimura A, Udaka J;

PI

XX WPI; 1991-369253/50.

DR

DR P-PSDB; AAR15471.

XX

PT Expression vector for signal peptide from Bacillus brevis - for

PT expression of interferon, insulin, epidermal growth factor etc.

PT with improved yield

XX

PS Disclosure; Fig 3A-B; 44pp; Japanese.

XX

CC DNA encoding the signal peptide associated with the BBRP42 gene of B.

CC brevis may be incorporated into an expression vector, pref. with

CC the promoter sequence and transcription control region as indicated

CC in the features. DNA encoding a foreign protein may be ligated

CC immediately downstream of the signal region. The vector may then be

CC used to transform a host organism which then expresses the protein

CC on culture. BBRP42 is secreted by B. brevis during an early stage

CC of incubation, and so its associated signal peptide allows a foreign

CC protein to be secreted during this early stage when protease prodn.

CC is low, thus increasing recovery of the protein. Proteins for which

CC the method may be used include interferon, interleukin, human

CC epidermal growth factor, GM-CSF, Factor VIII, insulin, tumour

CC necrosis factor and NGF.

CC See also AAQ15229-31.

XX

SQ Sequence 1796 BP; 603 A; 359 C; 490 G; 344 T; 0 other;

Query Match 13.8%; Score 28.4; DB 12; Length 1796;

Best Local Similarity 58.1%; Pred. No. 21;

Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 103 TTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTTCACGACACT 162

Db 764 TTGGAGTTTATCGGCATCCAGCTTCAAGAGAGACAGCAGTTCTTCGTTTTCTCGAAGCC 705

QY 163 TCCAAGGACGCCATACCGAACAAAGC 188

Db 704 ACCGATGAAGCCTCCTCTGCGGAAGC 679

RESULT 37

AAH67141

ID AAH67141 standard; DNA; 3012 BP.

XX

AC AAH67141;

XX

DT 26-SEP-2001 (first entry)

XX

DE C glutamicum coding sequence fragment SEQ ID NO: 2176.

XX

KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

KW organic acid synthesis; ds.

XX

OS Corynebacterium glutamicum.

XX

PN EP1108790-A2.

XX

PD 20-JUN-2001.

XX

PF 18-DEC-2000; 2000EP-0127688.

XX

PR 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

XX

PA (KYOW) KYOWA HAKKO KOGYO KK.

XX

PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX

DR WPI; 2001-376931/40.

DR P-PSDB; AAG91922.

XX

PT Novel polynucleotides derived from Coryneform bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analysing

PT expression profile or pattern of a gene and identifying homologous gene
PT
XX
PS Claim 8; SEQ ID NO: 2176; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of corynebacterium bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
CC from corynebacterium bacterium. Corynebacterium bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 3012 BP; 676 A; 877 C; 891 G; 568 T; 0 other;

Query Match 13.8%; Score 28.4; DB 22; Length 3012;
Best Local Similarity 60.3%; Pred. No. 26;
Matches 47; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GCTCGAGCCATGGTATGGACGTATACAGGTTCTTGGTCAATTTCCAGGACACACATGATT 60
Db 1598 GCATTACCCAGGGCATTTGGTGCATACACAGGTCAGGTAAGTTAAATGTCGAGGACATGAGCGCA 1657

QY 61 CGGTCCAAGAACAGGATA 78
Db 1658 CGATCACCTTCTGGATA 1675

RESULT 38
ABL21316/c
ID ABL21316 standard; DNA; 3045 BP.
XX
AC ABL21316;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15421.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 15421; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3045 BP; 856 A; 726 C; 698 G; 765 T; 0 other;

Query Match 13.8%; Score 28.4; DB 23; Length 3045;
Best Local Similarity 52.5%; Pred. No. 26;
Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 48 GACACAGATGATTGGTCCAGAACAGGATAATAGAACTAAGCAACGCGATACATTGG 107
Db 880 GATACCAAGTATTTCATTCTATAAACTGTAAACTGGCACCCACGCCCAATAATTCGA 821

QY 108 GTGGATTGGCAACAACTTCTGTGACTAACAGGTCCATAGTTTTTACGACACTTCC 165
Db 820 AACGAAATAAATAAACCCGTTGCCATTGACTAACTAACTTTTACAAGAGATTTC 763

RESULT 39
AAQ53462
ID AAQ53462 standard; DNA; 3946 BP.
XX
AC AAQ53462;
XX
DT 20-JUN-1994 (first entry)
XX
DE BaMMV coat protein gene.
XX
KW Barley mild mosaic virus; diagnosis; barley yellow mosaic disease;
KW disease resistant barley; ss.
XX
OS Barley mild mosaic virus strain Kal.
XX
FH Key Location/Qualifiers
FT CDS 1..3609
FT /*tag= a
FT misc_RNA 2854..3606
FT /*tag= b
FT /*note= "BaMMV strain Kal coat protein"
XX
PN EP574878-A.
XX
PD 22-DEC-1993.
XX
PF 15-JUN-1993; 93EP-0109531.
XX
PR 16-JUN-1992; 92JP-0180624.
XX
PA (NORQ) JAPAN MIN AGRIC FORESTRY.
PA (SAPB) SAPPORO BREWERIES.
XX
PI Hibino H, Ito K, Kashiwazaki S, Kuroda H;
XX
DR WPI; 1993-407253/51.
DR P-PSDB; AAR44507.
XX
PT New DNA sequences encoding barley mild mosaic virus coat protein
PT - useful for diagnosis and prepn. of resistant strains
XX
PS Claim 1; Page 14-23; 25pp; English.
XX
CC The sequence is that of a coat protein gene of barley mild mosaic
CC virus (BaMMV). The determ. of the genetic structure of BaMMV
CC coat proteins may contribute to the diagnosis of the virus which
CC causes barley yellow mosaic disease, as well as to the prodn. of
CC yellow mosaic-disease resistant barley utilising BaMMV coat protein
CC genes.

XX SQ Sequence 3946 BP; 1110 A; 1059 C; 891 G; 886 T; 0 other;

Query Match 13.8%; Score 28.4; DB 14; Length 3946;
Best Local Similarity 54.9%; Pred. No. 29;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 6 AGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGTCGTC 65
Db 612 AGGCATGACCATGAACCCATGAGTTCTTTCCACCATTCACAGCGCAAGATGGTGGCTT 671

QY 66 CAAGACAGGATAATAGAACTAAGCAACGCGATACAAATTGG 107
Db 672 CATCAAGACCGCAAAAGACACACTCAACTGCATCCTTACGG 713

RESULT 40
ABL21314/c
ID ABL21314 standard; DNA; 4407 BP.

XX AC ABL21314;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15415.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ds.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS Claim 1; SEQ ID NO 15415; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins
XX CC (ABB57737-ABB72072).

XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 4407 BP; 1332 A; 955 C; 917 G; 1203 T; 0 other;

Query Match 13.8%; Score 28.4; DB 23; Length 4407;
Best Local Similarity 52.5%; Pred. No. 30;
Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 48 GACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAAGCAACCGCATCAATTGG 107
Db 3726 GATACCAAGTATTTCATTATATAAACTGTAACTGGCACCCACGCCACGAAATAATTGCA 3667

QY 108 GTGATTGGCAACAACCTTCTGTGACTAACAGGTCCATAGTTTTCACGACACTTCC 165
Db 3666 AACGAAAATAAATAAACCCGTTGCCATTGACTAAACTAACTTTTACAAGAGATTTC 3609

RESULT 41
AAH68530/c
ID AAH68530 standard; DNA; 349980 BP.

XX AC AAH68530;
XX DT 26-SEP-2001 (first entry)
XX DE C glutamicum coding sequence fragment SEQ ID NO: 7065.
XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX KW organic acid synthesis; ds.
XX OS Corynebacterium glutamicum.
XX PN EP1108790-A2.
XX PD 20-JUN-2001.
XX PF 18-DEC-2000; 2000EP-0127688.
XX PR 16-DEC-1999; 99JP-0377484.
XX PR 07-APR-2000; 2000JP-0159162.
XX PR 03-AUG-2000; 2000JP-0280988.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX WPI; 2001-376931/40.

XX PT Novel polynucleotides derived from Coryneform bacteria, for identifying
XX PT mutation point of a gene, measuring expression of a gene, analysing
XX PT expression profile or pattern of a gene and identifying homologous gene
XX PT -
XX PS Disclosure; SEQ ID NO: 7065; 246pp + Sequence Listing; English.
XX CC The present invention provides a number of nucleotide and protein
XX CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX CC are useful for identifying the mutation point of a gene derived from a
XX CC mutant of coryneform bacterium, measuring expression amount and
XX CC analysing the expression profile or expression pattern of a gene derived
XX CC from Coryneform bacterium, and identifying a homologue of a gene derived
XX CC from coryneform bacterium. Coryneform bacteria are useful for producing
XX CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
XX CC particularly L-lysine. The present sequence is a nucleic acid described
XX CC in the exemplification of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC European Patent Office.

XX SQ Sequence 349980 BP; 86896 A; 98023 C; 80939 G; 84122 T; 0 other;

Query Match 13.8%; Score 28.4; DB 22; Length 349980;
Best Local Similarity 60.3%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATT 60
Db 295126 GCATTACCCAGGGCATTGGTGCATACCAGGTCAAGGTAAATGTGCGAGCAGACTGAGCGCA 295067

QY 61 CGGTCCAAGAACAGGATA 78
Db 295066 GCATCACCTTCTCTGGATA 295049

RESULT 42
AAC01804/c
ID AAC01804 standard; cDNA; 383 BP.
XX
AC AAC01804;
XX
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 1802.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
DR P-PSDB; AAG01798.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 1802; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors.
XX
SQ Sequence 383 BP; 100 A; 82 C; 88 G; 111 T; 2 other;

Query Match 13.7%; Score 28.2; DB 21; Length 383;
Best Local Similarity 51.2%; Pred. No. 14;
Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 9 CATGGTATGACCTATACGAGTTCTTGGTCAATTTCAGGACACAGATGATTCGGTCCAA 68
Db 217 CTTGTTGTCAACACAGATGATCCCCAGGTCAAATTTCTGCACCTCTAAATCCTCCTTAC 158

QY 69 GAACAGGATATAGAACTAAGCAACGCCGATACAAATTTGGGTGGATTGGCAACAACTTCC 128
Db 157 AATCTCGATCTTACTGCGAAGTGGCGCTCTCCTGTATGGGGATGACTCGCTGCAGATTCT 98

QY 129 TGTGACTAA 137
Db 97 AATCACCAC 89

RESULT 43
AAZ33507/c

ID AAZ33507 standard; cDNA; 501 BP.
XX
AC AAZ33507;
XX
DT 08-DEC-1999 (first entry)
XX
DE Human prostate cancer-associated EST 31.
XX
KW Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;
KW cancer; tissue specificity; human; ss.
XX
OS Homo sapiens.
XX
PN DE19811194-A1.
XX
PD 16-SEP-1999.
XX
PF 10-MAR-1998; 98DE-1011194.
XX
PR 10-MAR-1998; 98DE-1011194.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX
DR WPI; 1999-519629/44.
DR P-PSDB; AAY48371.
XX
PT New nucleic acid expressed at high level in normal prostatic tissue and
PT encoded polypeptides, used to treat cancer and screen for therapeutic
PT agents -
XX
PS Claim 1a; 99; 194pp; German.
XX
CC This invention describes novel nucleic acid sequences (A) that are
CC expressed at high level in normal prostatic tissue. Polypeptides (I)
CC encoded by (A) are used: (a) for identifying agents for treatment of
CC prostatic cancer and (b) for therapy of prostate cancer, optionally
CC where expressed by gene therapy methods. (A) is also used to isolate
CC full-length genes (for gene therapy) and for recombinant production of
CC (I), which can be used to raise specific antibodies. (A) are identified
CC by assembly of ESTs (expressed sequence tags) before these are analyzed
CC for expression pattern (tissue specificity). This approach eliminates
CC many of the false results, as regards tissue specificity, associated
CC with known methods that use single (usually short) ESTs. AAZ33477-233540
CC represent expressed sequence tags described in the method of the
CC invention.
XX
SQ Sequence 501 BP; 122 A; 120 C; 125 G; 134 T; 0 other;

Query Match 13.7%; Score 28.2; DB 20; Length 501;
Best Local Similarity 51.2%; Pred. No. 16;
Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 9 CATGGTATGACCTATACGAGTTCTTGGTCAATTTCAGGACACAGATGATTCGGTCCAA 68
Db 296 CTTGTTGTCAACACAGATGATCCCCAGGTCAAATTTCTGCACCTCTAAATCCTCCTTAC 237

QY 69 GAACAGGATATAGAACTAAGCAACGCCGATACAAATTTGGGTGGATTGGCAACAACTTCC 128
Db 236 AATCTCGATCTTACTGCGAAGTGGCGCTCTCCTGTATGGGGATGACTCGCTGCAGATTCT 177

QY 129 TGTGACTAA 137
Db 176 AATCACCAC 168

RESULT 44
AAK99319/c
ID AAK99319 standard; cDNA; 652 BP.
XX
AC AAK99319;
XX

DT	11-JUN-2002	(first entry)
XX		
DE	cDNA encoding ferritin 14 protein.	
XX		
KW	Ferritin 14 protein; DNA recombination; antagonist; malignant tumour; haemopathy; HIV infection; immunological disease; inflammation; gene; ss.	
XX		
OS	Unidentified.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	193..567
FT	/*tag= a	
FT	/product= "Protein of ferritin 14"	
XX		
PN	CN1324811-A.	
XX		
PD	05-DEC-2001.	
XX		
PF	24-MAY-2000; 2000CN-0115822.	
XX		
PR	24-MAY-2000; 2000CN-0115822.	
XX		
PA	(BODE-) BODE GENE DEV CO LTD SHANGHAI.	
XX		
PI	Mao Y, Xie Y;	
XX		
DR	WPI; 2002-281644/33.	
DR	P-PSDB; AAO20447.	
XX		
PT	Polypeptide ferritin 14, for curing diseases such as malignant tumor, hemopathy, HIV infection, immunological disease and various inflammations -	
PT		
XX		
PS	Claim 6; Page 24 Disclosure; 31pp; Chinese.	
XX		
CC	The invention relates to a novel ferritin 14 protein, the encoding polynucleotide, the production of the polynucleotide using DNA recombination, and an antagonist against the polynucleotide. The polynucleotide of the invention is useful for curing diseases such as malignant tumours, haemopathy, HIV infections, immunological disease and various inflammations. This polynucleotide sequence represents the cDNA encoding the ferritin 14 protein of the invention.	
XX		
SQ	Sequence 652 BP; 140 A; 174 C; 202 G; 136 T; 0 other;	
Query Match		
Best Local Similarity 13.7%; Score 28.2; DB 24; Length 652;		
Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0		
QY	9	CATGGTATGGACGTATACGAGTCTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68
Db	327	CTTGTGTGCAACACAGATGATCCCGAGGTCAAAATTTCTGCACTCTCTAAATCCTCCTTAC 268
QY	69	GAACAGGATATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCC 128
Db	267	AATCTCGATCTACTGCGAAGTGGCGCTCTCCTGATGGGATGACTCGCTGCAGATTTCT 208
QY	129	TGTGACTAA 137
Db	207	AATCACCACAA 199
RESULT 45		
AAH99764		
ID	AAH99764 standard; cDNA; 716 BP.	
XX		
AC	AAH99764;	
XX		
DT	16-OCT-2001 (first entry)	
XX		
DE	Human protein encoding cDNA sequence SEQ ID NO:599.	
XX		
KW	Human; cancer; ulcer; HIV infection; human immunodeficiency virus;	

Db 563 AATCTCGATCTTACTGCGAAGTGGGCTCTCCTGATGGGATGACTCGCTGCAGATTCT 622

Qy 129 TGIGACTAA 137

Db 623 AATCACCA 631

RESULT 46

ABA05428/c

ID ABA05428 standard; cDNA; 1514 BP.

XX

AC ABA05428;

DT 28-FEB-2002 (first entry)

XX

DE Human RetinaxR encoding cDNA SEQ ID NO 1.

XX

KW Human; RetinaxR; antidiabetic; anorectic; ophthalmological; antigout;

KW antiinflammatory; immunostimulant; nuclear receptor; diabetes; obesity;

KW age-related macular degeneration; retinopathy; conjunctivitis; gout;

KW DiGeorge's syndrome; retinitis pigmentosa; neovascular glaucoma;

KW corneal inflammation; severe combined immunodeficiency disease; SCID;

KW dermatomyositis; gene therapy; gene expression; gene; ss.

XX

OS Homo sapiens.

XX

FH Key

FT CDS

FT 19..1251

FT /tag= a

FT /product= "RetinaxR"

FT 19..156

FT /tag= b

FT /note= "Encodes the amino-terminal A/B domain, claim 11"

FT 157..351

FT /tag= c

FT /note= "Encodes the DNA binding domain, claim 9"

FT 352..1251

FT /tag= d

FT /note= "Encodes the ligand binding domain, claim 7"

XX

PN WO200183556-A2.

XX

PD 08-NOV-2001.

XX

PF 04-MAY-2001; 2001WO-US14601.

XX

PR 04-MAY-2000; 2000US-201874P.

XX

PA (GLAX) GLAXO GROUP LTD.

XX

PI Moore JT;

XX

DR WPI; 2002-049337/06.

DR P-PSDB; AAM47934.

XX

PT Novel nuclear receptor, Retinax receptor polypeptide, useful for

PT identifying modulators of the receptor which are used for treating

PT diabetes, obesity, age-related macular degeneration, gout,

PT conjunctivitis -

XX

PS Claim 13; Page 28; 30pp; English.

XX

CC The invention relates to an isolated nuclear receptor, Retinax receptor

CC (RetinaxR) polypeptide with antidiabetic, anorectic, ophthalmological,

CC antigout, antiinflammatory and immunostimulant activity. RetinaxR is

CC useful for screening a compound for its ability to inhibit or activate

CC RetinaxR nuclear receptor, as a diagnostic agent for diagnosing patients

CC having a predisposition to diabetes and/or obesity, for monitoring

CC patient's response to treatment of diabetes or obesity, for treating a

CC subject having a disorder that is responsive to RetinaxR receptor

CC modulation e.g. diabetes, obesity and age-related macular degeneration,

CC for treating retinopathies e.g. diabetic retinopathy, conjunctivitis,

CC DiGeorge's syndrome, retinitis pigmentosa, neovascular glaucoma, corneal

CC inflammation, severe combined immunodeficiency disease, gout,

CC dermatomyositis, etc. Nucleic acids encoding RetinaxR are also useful for

CC treating the above mentioned disorders by gene therapy. The present

CC sequence is that of the RetinaxR encoding cDNA sequence.

XX

SQ Sequence 1514 BP; 352 A; 446 C; 424 G; 292 T; 0 other;

Query Match 13.7%; Score 28.2; DB 24; Length 1514;

Best Local Similarity 57.3%; Pred. No. 24;

Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACATTTGGTGGATTGGCAACAAA 123

Db 1462 TACCACAACTTGTTAATTCTCTACCATCAATATACAGTTTGGGCTATTATGAATAAA 1403

Qy 124 CTTCTGTGACTAACAACAGGTCCATAGTTT 152

Db 1402 GCTGCTATGAATATCTTACAATATCTTT 1374

RESULT 47

AAZ61225/c

ID AAZ61225 standard; DNA; 1920 BP.

XX

AC AAZ61225;

XX

DT 30-MAY-2000 (first entry)

XX

DE Human retinal nuclear receptor consensus RACE sequence.

XX

KW Human; retinal orphan nuclear hormone receptor; splice variant;

KW hRetinOR2; hRetinOR1; retina; response element;

KW hormone-mediated homeostasis; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO200008052-A1.

XX

PD 17-FEB-2000.

XX

PF 06-AUG-1999; 99WO-US17885.

XX

PR 07-AUG-1998; 98US-0130858.

XX

PA (TULA-) TULARIK INC.

XX

PI De La Brousse-Elwood FC;

XX

DR WPI; 2000-195554/17.

XX

PT Human retinal nuclear hormone receptor and coding sequences, useful for

PT identifying ligands and response elements involved in homeostasis -

XX

PS Disclosure; Fig 1; 58pp; English.

XX

CC The present sequence represents a consensus RACE sequence of human

CC retinal orphan nuclear hormone receptor variants hRetinOR2 and hRetinOR1.

CC The two hRetinOR polynucleotides are identical, except that hRetinOR2

CC includes a 40 bp insertion following nucleotide 1188. This insertion,

CC which is due to a mRNA splicing variation, introduces a stop codon into

CC the hRetinOR2 polynucleotide, which results in a truncated hRetinOR2

CC polypeptide. The polynucleotides are expressed only in the retinal

CC tissues. The nuclear hormone receptors are found in retinal cells, and

CC are useful for identifying ligands that can modulate their activity and

CC for identifying response elements that are responsive to the nuclear

CC hormone receptors. The receptors and methods are useful for research of

CC hormone-mediated homeostasis.

XX

SQ Sequence 1920 BP; 480 A; 514 C; 536 G; 390 T; 0 other;

Query Match 13.7%; Score 28.2; DB 21; Length 1920;

Best Local Similarity 57.3%; Pred. No. 26;


```

CC homeostasis.
XX
SQ Sequence 1960 BP; 480 A; 523 C; 539 G; 401 T; 17 other;

Query Match 13.7%; Score 28.2; DB 21; Length 1960;
Best Local Similarity 57.3%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 64 TCCAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAA 123
Db 1571 TACCACAACTTGTTAATTCATCCCTACCATCAATATACAGTTTGGGGCTATTATGAATAAA 1512

QY 124 CTTCTGTGACTAACAGGTCCATAGTTTT 152
Db 1511 GCTGCTATGAATATTCTTACAATATCTTT 1483

RESULT 50
AAZ61236/c
ID AAZ61236 standard; DNA; 1978 BP.
XX
AC AAZ61236;
XX
DT 30-MAY-2000 (first entry)
XX
DE Human retinal nuclear receptor consensus DNA sequence.
XX
KW Human; retinal orphan nuclear hormone receptor; splice variant;
KW hRetinOR2; hRetinOR1; retina; response element;
KW hormone-mediated homeostasis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200008052-A1.
XX
PD 17-FEB-2000.
XX
PF 06-AUG-1999; 99WO-US17885.
XX
PR 07-AUG-1998; 98US-0130858.
XX
PA (TULA-) TULARIK INC.
XX
PI De La Brousse-Elwood FC;
XX
DR WPI; 2000-195554/17.
XX
PT Human retinal nuclear hormone receptor and coding sequences, useful for
PT identifying ligands and response elements involved in homeostasis -
XX Disclosure; Fig 1; 58pp; English.
XX
CC The present sequence represents a consensus sequence of human retinal
CC orphan nuclear hormone receptor variants hRetinOR2 and hRetinOR1.
CC The two hRetinOR polynucleotides are identical, except that hRetinOR2
CC includes a 40 bp insertion following nucleotide 1188. This insertion,
CC which is due to a mRNA splicing variation, introduces a stop codon into
CC the hRetinOR2 polynucleotide, which results in a truncated hRetinOR2
CC polypeptide. The polynucleotides are expressed only in the retinal
CC tissues. The nuclear hormone receptors are found in retinal cells, and
CC are useful for identifying ligands that can modulate their activity and
CC for identifying response elements that are responsive to the nuclear
CC hormone receptors. The receptors and methods are useful for research of
CC hormone-mediated homeostasis.
XX
SQ Sequence 1978 BP; 475 A; 528 C; 536 G; 398 T; 41 other;

Query Match 13.7%; Score 28.2; DB 21; Length 1978;
Best Local Similarity 57.3%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAA 123

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09-833799-13c.rng

Sun Feb 16 09:13:51 2003

QY 115 GGCAACAAACTTCTGTGACTAAGAGGTCATAGTTTTCACGAC 159
Db 66 GATTACCAATTGTGATGTAGGATCCCAATCATAGTATTTAAGCAC 22

RESULT 52
AAQ10484/c
ID AAQ10484 standard; cDNA; 2385 BP.
XX AC AAQ10484;
XX 22-APR-1991 (first entry)
DE Encodes Feline calicivirus capsid protein.
XX feline calicivirus capsid protein; FCV; multivalent vaccine; cat; ds.
XX feline calicivirus.
OS
XX
FH Key Location/Qualifiers
FT CDS 18..2024
FT /*tag= a
FT /product= capsid protein

XX WO9101332-A.
PN
XX
XX 07-FEB-1991.
PD
XX
XX 09-JUL-1990; 90WO-US03753.
PF
XX 21-JUL-1989; 89US-0383909.
PR
XX 18-SEP-1989; 89US-0408989.
PR
XX (UPJO) UPJOHN CO.
PA
XX
XX Wardley R, Post LE;
PI
XX WPI; 1991-058117/08.
DR
XX P-PSDB; AAR10686.
DR
XX Feline calicivirus capsid protein - from recombinant DNA for subunit
PT and multivalent vaccines for FCV
PT
XX
PS Claim 3; Page 28; 40pp; English.

XX CRFK cells were inoculated, total poly-A+ RNA was isolated and FCV
CC double-stranded RNA was LiCl fractionated from this RNA. Double-
CC stranded cDNA was prepared, blunt-ended with t4 DNA polymerase and
CC treated with EcoRI methylase prior to ligation of EcoRI linkers. The
CC mixture was digested with EcoRI and ligated to lambda gt10. E.coli
CC strains transformed with the viral vectors were plated and positive
CC plaques were transferred to nitrocellulose. They were probed with
CC random-primed cDNA prepared from FCV genomic RNA. A plaque with a
CC strong hybridisation signal was isolated and found to contain an
CC EcoRI fragment (ca.4200bp). It was cloned in pUC18 to give pCV2.
CC A second library was constructed in pUC18 using PstI linkers. A
CC plasmid was selected from this library and designated pCV7. It was
CC found to have restriction sites in common with pCV2. These two
CC plasmids were used to isolate other regions of the FCV genome.
XX
SQ Sequence 2385 BP; 642 A; 562 C; 502 G; 679 T; 0 other;

Query Match 13.7%; Score 28.2; DB 12; Length 2385;
Best Local Similarity 54.3%; Pred. No. 28;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 55 ATGATTCGGTCCAAAGACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGIGGATT 114
Db 143 AGGATAAACAACACATTAAGGGTTATCGCAGAACCCACATGTAGAAATTTGTTGGGGTT 84
QY 115 GGCAACAAACTTCTGTGACTAAGAGGTCATAGTTTTCACGAC 159
Db 83 GATTACCAATTGTGATGTAGGATCCCAATCATAGTATTTAAGCAC 39

RESULT 53
AAQ94444
ID AAQ94444 standard; DNA; 5009 BP.
XX
XX AC AAQ94444;
XX 09-OCT-1996 (first entry)
DE Bacterial transferrin receptor operon (H. influenzae strain MinnA).
XX
KW Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen;
KW non-typable strain; Haemophilus influenzae; meningitis; ss.
XX
OS Haemophilus influenzae strain MinnA.
XX
FH Key Location/Qualifiers
FT CDS 121..2103
FT /*tag= a
FT /product= Tbp2
FT 2117..4856
FT /*tag= b
FT /product= Tbp1

XX WO9513370-A1.
PN
XX 18-MAY-1995.
PD
XX
XX 07-NOV-1994; 94WO-CA00616.
PF
XX 29-DEC-1993; 93US-0175116.
PR
XX 08-NOV-1993; 93US-0148968.
PR
XX (CONN-) CONNAUGHT LAB LTD.
PA
XX Chong P, Gray-owen S, Harkness R, Klein M, Loosmore S;
PI Murdin A, Schryvers A, Yang Y;
PI
XX WPI; 1995-194089/25.
DR
XX P-PSDB; AAR77887-88.
DR
XX Nucleic acids encoding Haemophilus transferrin receptor - used to
PT develop prods for detection and in diagnosis, prevention and
PT treatment of Haemophilus infection.
PT
XX Claim 12; Fig 5A-Q; 231pp; English.

XX The present DNA shows the transferrin receptor (Tfr) operon consisting of
CC two genes (Tbp1 and Tbp2) arranged in tandem and which are transcribed
CC from a single promoter, from Haemophilus influenzae type b, strain MinnA.
CC H. influenzae Tfr is iron- and/or haemin-regulated and a putative fur-
CC binding site has been identified upstream of tbp2. Antibodies blocking
CC this binding site may prevent bacterial growth. Fragments of the Tfr
CC (or its genes) are useful in vaccines to provide protection against, e.g.
CC bacterial meningitis. An advantage of using the Tfr is that it shares
CC homology with Tfr of other H. influenzae strains including non-typable
CC strains.

XX SQ Sequence 5009 BP; 1809 A; 835 C; 935 G; 1430 T; 0 other;
Query Match 13.7%; Score 28.2; DB 16; Length 5009;
Best Local Similarity 64.6%; Pred. No. 36;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 142 TCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAAGCGTGTATTAT 201
Db 1579 TTCTTATTAGTACCGTACTCCCAAGGACGACATACCTAAACAGGAAGTGCAAAATAT 1638
QY 202 CCTAG 206
Db 1639 CATGG 1643

Sun Feb 16 09:13:51 2003

0;

Db 1579 TTCTATTAGGTACCGTACTCCCAAGGACGACATACCTATAAACAGGAAGTGCAAAATAT 1638
QY 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 56
AAZ89158
ID AAZ89158 standard; DNA; 5009 BP.
XX AAZ89158;
DT 13-JUN-2000 (first entry)
DE H. influenzae type B strain Minna DNA containing Tbp1 and Tbp2.
XX Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
KW diagnosis; ds.
XX Haemophilus influenzae.

Key Location/Qualifiers
CDS 121..2103
/*tag= a
/product= "Tbp1"
2117..4855
/*tag= b
/product= "Tbp2"
US6015688-A.
18-JAN-2000.
07-JUN-1995; 95US-0483577.
08-NOV-1994; 94US-0337483.
08-NOV-1993; 93US-0148968.
29-DEC-1993; 93US-0175116.
(CONN-) CONNAUGHT LAB LTD.
Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
Murdin A, Klein M, Chong P;
WPI; 2000-181144/16.
P-PSDB; AAY51691, AAY51692.
New nucleic acid encoding truncated transferrin receptor, useful for
diagnosis, treatment and prevention of bacterial infections,
particularly by Haemophilus -
Example 4; Column 65-76; 281pp; English.
This invention describes a novel isolated and purified nucleic acid (I)
encoding an immunogenic, C-terminally truncated analog of one of the
transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae
which has antibacterial activity. (I) are used for recombinant
production of truncated Tbp; as probes and primers for detecting, and
diagnosing infection by, Haemophilus, also for isolating similar
sequences from other bacteria; as immunogens for vaccinating against
infections caused by bacteria that produce transferrin receptors, e.g.
Haemophilus, Neisseria or Branhamella. The truncated proteins are useful
as immunogens (as above); for diagnosing infection (as antigens in
immunoassays) and for raising antibodies, used for diagnosis of
infections or for passive immunization. This sequence encodes the
transferrin receptor proteins Tbp1 and Tbp2 isolated from H. influenzae
type B strain Minna.
XX Sequence 5009 BP; 1809 A; 836 C; 934 G; 1430 T; 0 other;
SQ Query Match 13.7%; Score 28.2; DB 21; Length 5009;
Best Local Similarity 64.6%; Pred. No. 36;

Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 142 TCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAGGTTATTAT 201
Db 1579 TTCTATTAGGTACCGTACTCCCAAGGACGACATACCTATAAACAGGAAGTGCAAAATAT 1638

QY 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 57
AAZ91000
ID AAZ91000 standard; DNA; 5009 BP.
XX AAZ91000;
DT 06-JUN-2000 (first entry)
DE H. influenzae type B strain Minna transferrin receptor gene.
XX Antibacterial; antiinflammatory; auditory; respiratory; antibody;
KW antiserum; transferrin receptor; immunogen; epitope; otitis media;
KW bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis; ds.
XX Haemophilus influenzae.

Key Location/Qualifiers
CDS 121..2103
/*tag= a
/product= "Tbp1 protein"
2117..4855
/*tag= b
/product= "Tbp2 protein"

US6008326-A.
28-DEC-1999.
07-JUN-1995; 95US-0474671.
08-NOV-1995; 95US-0337483.
08-NOV-1993; 93US-0148968.
29-DEC-1993; 93US-0175116.
(CONN-) CONNAUGHT LAB LTD.
Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;
Murdin A, Schryvers A;
WPI; 2000-096387/08.
P-PSDB; AAY80357, AAY80358.
Antibodies specific for transferrin receptor proteins of Haemophilus
influenzae, useful for treating otitis media, epiglottitis, pneumonia
and tracheobronchitis -
Claim 4; Fig 5; 252pp; English.
The invention relates to novel antibodies (or monospecific antisera)
specific for single transferrin receptor proteins (or immunogenic
fragment) from strains of Haemophilus influenzae. This sequence
corresponds to the coding sequences for the Tbp1 and Tbp2 transferrin
receptor proteins from H. influenzae type B strain Minna. The antibodies
may be used for preventing and treating infections and disorders caused
by H. influenzae, including bacterial meningitis, otitis media,
epiglottitis, pneumonia and tracheobronchitis. The antibodies may also
be used to detect the presence of H. influenzae proteins in samples
according to standard methodologies (e.g. enzyme linked immunosorbant
assay (ELISA)) and hence diagnose infections.
XX Sequence 5009 BP; 1809 A; 836 C; 934 G; 1430 T; 0 other;
SQ

Query Match	13.7%	Score 28.2;	DB 21;	Length 5009;
Best Local Similarity	64.6%	Pred. No. 36;		
Matches 42;	Conservative	0;	Mismatches 23;	Indels 0;
				Gaps 0;

Qy	142	TC	CA	TAG	TTTT	TT	CA	GA	CA	CT	TC	CA	AG	GC	GC	CA	TAC	CG	GA	CA	AA	AG	CA	AG	GT	GT	TAT	TAT	201
D _b	1579	TT	CT	TAT	T	AG	GT	CA	CG	TAC	T	CC	CA	AG	GC	GC	TAC	CT	TA	AA	AC	AG	GA	AG	TG	CA	AA	AAT	1638

Qy	202	CCTAG	206
Db	1639	CATGG	1643

RESULT 58
AAQ94443
ID AAQ94443 standard; DNA: 5033 BP.

AA
AC
AAQ94443;

DT 09-OCT-1996 (first entry)

DE Bacterial transferrin receptor operon (H. influenzae strain Eagan).

Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen; non-typable strain; Haemophilus influenzae; meningitis; ss.

OS Haemophilus influenzae strain Eaqa.

PH	Key	Location/Qualifiers
FT	CDS	169..2151
FT		/*tag= a
FT		/product= Tbp2
FT	CDS	2165..4904
FT		/*tag= b
FT		/product= Tbp1

PN WO9513370-A1.

PD 18-MAY-1995.

PF 07-NOV-1994; 94WO-CA00616.

PR 29-DEC-1993; 93US-0175116.

PR 08-NOV-1993; 93US-0148968:

PA (CONN-) CONNAUGHT LAB LTD.

PI Chong P, Gray-owen S, Harkness R, Klein M, Loosmore S;
PI Murdin A, Schryvers A, Yang Y;

DR WPI; 1995-194089/25.
DR P-PSDB; AAR77885-86.

PT Nucleic acids encoding Haemophilus transferrin receptor - used to
PT develop prods for detection and in diagnosis, prevention and
PT treatment of Haemophilus infection.

PS Claim 12; Fig 4A-Q; 231pp; English.

The present DNA shows the transferrin receptor (TfR) operon consisting of two genes (Tbp1 and Tbp2) arranged in tandem and which are transcribed from a single promoter, from *Haemophilus influenzae* type b, strain Eagan. *H. influenzae* TfR is iron- and/or haemin-regulated and a putative fur-binding site has been identified upstream of *tbp2*. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the TfR (or its genes) are useful in vaccines to provide protection against, e.g. bacterial meningitis. An advantage of using the TfR is that it shares homology with TfR of other *H. influenzae* strains including non-typable strains.

SQ Sequence 5033 BP; 1822 A; 840 C; 937 G; 1434 T; 0 other;

Query Match 13.7%; Score 28.2; DB 16; Length 5033;

Best Local Similarity 64.6%; Pred. No. 36;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 142 TCCATAGTTTTTTCAGCACACTTCCAAGGAGCGCATACCGAACAAAGCGTGTATTAT 201
Db 1627 TTCTTATTAGGTCACCGTACTCCCAAGGACGACATACCTTAAACACGGAAGTCGAAAATAT 1686

Qy	202	CCTAG	206
Db	1687	CATGG	1693

RESULT 59
AAT49501
ID AAT49501 standard; DNA: 5033 BP.

AC AAT49501;

DT 05-MAY-1998 (first entry)

Transferrin receptor gene sequence encoding Tbp1 and Tbp2.

Transferrin receptor; Haemophilus influenzae type b;
iron; human transferrin; iron source; antibody; bacterial growth; vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2; ss.

OS Haemophilus influenzae.

Key	Location/Qualifiers
FD	169..2151
FT	/*tag= a
FT	/note= "encodes Tbp2 (AAW08960)"
FT	2129..4903
FT	/*tag= b
FT	/note= "encodes Tbp1 (AAW08959)"

PN WO9640929-A2.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-CA00399.

PR 17-MAY-1996; 96US-0649518.

PR 07-JUN-1995; 95US-0483577;
PR 07-JUN-1995; 95US-0483577;

PA (CONN-) CONNAUGHT LAB LTD.

Chong P, Gray-Owen S, Harkness RE, Klein MH, Loosmore SM;
PI
PI Murdin AD, Schryvers AB, Yang Y;

DR WPI; 1997-052329/05.
DR P-PSDB; AAW08959-60.

Haemophilus truncated transferrin receptor protein analogue, Tbp2
used to induce protection against disease caused by transferrin
producing pathogens, or as antigen to detect Haemophilus Tfr
antibodies

PS Claim 5; Fig 4A-Q; 228pp; English.

The present sequence represents the transferrin receptor gene of *Haemophilus influenzae* type b, strain Egan. The bacterial transferrin receptor is composed of 2 chains, Tbp1 and Tbp2. *H. influenzae* is a non-encapsulated or non-typable bacterium responsible for a wide range of human diseases. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The transferrin receptor, or fragments, therefore, are good vaccine candidates. The full length Tbp2 protein is produced in low amounts in *Escherichia coli*. However, the yield can be enhanced by truncation of the 3' end of the gene. An immunogenic composition comprising (or encoding) the immunogenic truncated analogue can be used to induce protection against a disease

caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunoassays for the detection of *Haemophilus* transferrin receptor antibodies, while the nucleic acid molecule can be used as a hybridisation probe for the detection of other transferrin receptor genes.

Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;

```
Query Match      13.7%; Score 28.2; DB 18; Length 5033;
Best Local Similarity 64.6%; Pred. NO. 36;
Matches 42; Conservative 0; Mismatches 23; Indels 0;
```

QY 142 TCCATAGTTTTTCACGACACTTCCAAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201

Db 1627 TTCCTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAAAACAGGAAGTGCAAAATAT 1686

QY 202 CCTAG 206
| | |
Db 1687 CATGG 1691

RESULT 60
AAV21429
ID AAV21429 standard: cDNA: 5033 BP.

AC	AAV21429;
XX	
DT	20-JUL-1998 (first entry)
XX	
DE	H. influenzae strain Eagan transferrin receptor operon.
XX	
KW	tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis;
KW	passive immunisation; ds.

XX	Haemophilus influenzae.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	169..2151	
FT		/*tag= a	
FT		/product= Tbp1	
FT		2165..4903	
FT	CDS	/*tag= b	
FT		/product= Tbp2	

XX	US5708149-A.	
PN		
XX		
PD	13-JAN-1998.	
XX		
PF	07-JUN-1995;	95US-0487890.
XX		
PR	08-NOV-1994;	94US-0337483.
PR	08-NOV-1993;	93US-0148968.
PR	29-DEC-1993;	93US-0175116.
PR	07-JUN-1995;	95US-0487890.

XX
PA
XX
PI
PI
XX

(CONN-) CONNAUGHT LAB LTD.

Chong P, Gray-Owen S, Harkness R, Klein M, Loosmore S;
Murdin A, Schryvers A, Yang Y;

WPI; 1998-100410/09.
P-PSDB; AAW53044. AAW53045.

Purification of recombinant Haemophilus transferrin-binding protein
- by solubilising inclusion bodies separated from cell lysate

Example 4: Fig 4: 261pp: English.

The H. influenzae transferrin receptor operon contains two genes (tbp1 and tbp2) under the transcriptional regulation of one promoter. The proteins encoded from these genes can be expressed in a recombinant host. The proteins can be used in vaccines against H. influenzae

```

CC infections or to produce antibodies for use in diagnosis or passive
CC immunisation.
XX
SQ Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;

Query Match      13.7%; Score 28.2; DB 19; Length 5033;
Best Local Similarity 64.6%; Pred. No. 36;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

```

QY 142 TCCATAGTTTTTCAGCACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201

Qy 202 CCTAG 206
| | |
Db 1687 CATGG 1691

RESULT 61
AAZ89157
ID AAZ89157 standard; DNA; 5033 BP.
XX
AC AAZ89157;

13-JUN-2000 (first entry)

xx Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
kw diagnosis; ds.

XX Haemophilus influenzae.

	Key	Location/Qualifiers
xx	CDS	169..2151
xx	FT	/*tag= a
xx	FT	/product= "Tbp1"
xx	FT	2165..4903
xx	FT	/*tag= b
xx	FT	/product= "Tbp2"

XX
PN US6015688-A.
XX
PD 18-JAN-2000.

XX	07-JUN-1995:	95US-0483577:
PF		

XX			
PR	08-NOV-1994;	94US-0337483.	
PR	08-NOV-1993;	93US-0148968.	
PD	28-DEC-1993.	93US-0175116.	

XX
52 (CONN-) CONNAUGHT LAB LTD.

XX Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
PI Mardin A, Klein M, Chong P;
PI

XX
DR WPI; 2000-181144/16.
DR P-PSDB: AAY51689, AAY51690.

XX New nucleic acid encoding truncated transferrin receptor, useful for
PT diagnosis, treatment and prevention of bacterial infections,
PT particularly by Haemophilus -
PT

XX
ps Example 4: Column 53-64; 281pp; English.

This invention describes a novel isolated and purified nucleic acid (I) encoding an immunogenic, C-terminally truncated analog of one of the transferrin receptor proteins Tbp1 or Tbp2 of *Haemophilus influenzae* which has antibacterial activity. (I) are used for recombinant production of truncated Tbp; as probes and primers for detecting, and diagnosing infection by, *Haemophilus*, also for isolating similar sequences from other bacteria; as immunogens for vaccinating against infections caused by bacteria that produce transferrin receptors, e.g.

The invention relates to novel antibodies (or monospecific antisera) specific for single transferrin receptor proteins (or immunogenic fragment) from strains of *Haemophilus influenzae*. This sequence

Db 2619 ATTGAAGAAGATATAAATAAGTAGAAATGTATTTTGAGTTGATGGATTGGAAAAATTATTA 2678
QY 131 TGACTAACAGGTCATAGTTTTCACGACACTT 163
Db 2679 TTATTAATAATGTTTTTAATATTTAAAGAAATTT 2711

RESULT 66
ABL26139
ID ABL26139 standard; DNA; 726 BP.
XX
AC ABL26139;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29890.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
Claim 1; SEQ ID NO 29890; 21pp + Sequence Listing; English.
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 726 BP; 173 A; 224 C; 200 G; 129 T; 0 other;

Query Match 13.6%; Score 28; DB 23; Length 726;
Best Local Similarity 51.6%; Pred. No. 21;
Matches 64; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 8 CCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCA 67
Db 350 CCATCGAGGTGACCTACAAGAGCACCAGTCCATATGGCTGGCCACAGATCCTGGTGACCG 409
QY 68 AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACCTTC 127
Db 410 TGTTCCGACGCAGTGGCCTGGGAGGAGACACTACTCGGTACGCTCACATCCACCTGC 469
QY 128 CTGT 131
Db 470 CCGT 473

RESULT 67
AAX03864/c
ID AAX03864 standard; DNA; 2007 BP.
XX
AC AAX03864;
XX
DT 07-APR-1999 (first entry)
XX
DE Feline calicivirus strain FCV 2280 capsid gene.
XX
KW Feline calicivirus; FCV; vaccine; capsid gene; infection;
KW splicing site; ss.
XX
OS Feline calicivirus.
XX
PN WO9856929-A1.
XX
PD 17-DEC-1998.
XX
PF 04-JUN-1998; 98WO-EP03326.
XX
PR 10-JUN-1997; 97US-0872056.
XX
PA (DIMM-) DIMMINACO AG.
XX
PI Colau D, Roos J;
XX
DR WPI; 1999-060333/05.
XX
PT Producing nucleic acid that is transcribed naturally in the
PT cytoplasm of eukaryotic cells - by altering consensus splicing
PT sites, specifically feline calicivirus capsid DNA for use in
PT vaccines
XX

Example 3; Fig 1; 72pp; English.

A method has been developed for the production of an isolated nucleic acid (I) that can be transcribed naturally in the cytoplasm of eukaryotic cells, without being altered by the splicing machinery. The method comprises modifying a consensus splicing site in (I). Also described in the present invention are: (1) isolated nucleic acid (Ia) containing a feline calicivirus (FCV) C gene with at least one modified or deleted consensus splicing site; (2) recombinant nucleic acid (II) comprising (Ia) fused to a sequence (III) encoding a polypeptide (IV); (3) vector that can express (I) in the nucleus of eukaryotic cells; and (4) cultures of cells infected with this vector. (II) and the vector of (3) are used in vaccines, specifically to treat or prevent FCV infections. Altering the splicing sites allows coding sequences to be transcribed in the nucleus of eukaryotic cells without alteration by the cells' natural splicing machinery, i.e. without changing the amino acid sequence of the expressed product. The present sequence represents Feline calicivirus strain FCV 2280 capsid gene from the present invention.

SQ Sequence 2007 BP; 528 A; 472 C; 416 G; 591 T; 0 other;

Query Match 13.6%; Score 28; DB 20; Length 2007;
Best Local Similarity 56.5%; Pred. No. 31;
Matches 52; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 68 AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACCTTC 127
Db 113 ATAAGAGGGTTATCACAAAAGCCCAACAGAAAGGAATTTGTTGGGTTGACAACTAATCTA 54
QY 128 CTGTACTAACAGGTCCTCATAGTTTTCACGAC 159
Db 53 AAGTGGGGATCCAGCCATAGTATTTAAGCAC 22

RESULT 68
ABL22422/c
ID ABL22422 standard; DNA; 2441 BP.

```

XX ABL22422;
AC AC
XX XX
XX 26-MAR-2002 (first entry)
XX DE
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 18739.
XX KW
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX OS
XX Drosophila melanogaster.
XX PN
XX WO200171042-A2.
XX PD
XX 27-SEP-2001.
XX PF
XX 23-MAR-2001; 2001WO-US09231.
XX PR
XX 23-MAR-2000; 2000US-191637P.
XX PR
XX 11-JUL-2000; 2000US-0614150.
XX PA
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Claim 1; SEQ ID NO 18739; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 2441 BP; 676 A; 517 C; 563 G; 685 T; 0 other;
SQ Query Match 13.6%; Score 28; DB 23; Length 2441;
Best Local Similarity 56.5%; Pred.No. 33;
Matches 52; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 47 GGACACAGATGATTCGGTCCAAGAACAAGGATAATAGAACTAAGCAACGCCGATACAATTG 106
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2362 GGCAACAGCAAATTAACAACCATTTACAATTATTGAACAACACGCCGCATGCAATGG 2303

Qy 107 GGTGGATTGGCAACAAACTTCCTGTGACTAAC 138
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2302 CGTGCCATGGCTCATAACTTCCAATGGCCACC 2271

RESULT 69
ABL08866
ID ABL08866 standard; cDNA; 3121 BP.
XX XX
AC ABL08866;
XX XX
DT 26-MAR-2002 (first entry)
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 21080.
DE Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
KW KW
XX XX
```


CC		abnormal cell proliferation and/or differentiation, these include
CC		thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,
CC		including breast cancer, sarcomas and other neoplasms, bladder cancer,
CC		colon cancer, lung cancer, prostate cancer, various leukaemias, and
CC		lymphomas. RBP-7 antibodies are useful as diagnostic agents.
XX		
SQ	Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other;	
	Query Match	13.6%; Score 28; DB 21; Length 162450;
	Best Local Similarity	53.7%; Pred. No. 1.5e+02;
	Matches	58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY	33 TTGGTCAATTTCAGGACACAGATGATTCGGTGCCAAGAACAAGATAAAGAACTAAGCAA	92
Dd	74432 TTAATCATTTCTCAATAAACGTGAGATCCTGTTGAGCATCAGAAAAAGGAAGAA	74491
QY	93 CGCGATACAATTTGGGTGGATTGGCAACAAAACCTTCTGTGACTAACAG	140
Dd	74492 GAGTATCTAATTTTAGTAGGTAGGCAGAAAAATGTAATTTCTAAATAG	74539
 RESULT 73 ABN63370/C		
ID	ABN63370 standard; cDNA; 505 BP.	
XX		
AC	ABN63370;	
XX		
DT	28-JUN-2002 (first entry)	
XX	Human cancer related polynucleotide SEQ ID NO 3337.	
DE		
XX		
KW	Human; cytostatic; gene expression; gene mapping; tissue profiling;	
KW	gene therapy; cancer; tumour; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PV	WO200214500-A2.	
PN		
XX		
PD	21-FEB-2002.	
XX		
PF	16-AUG-2001; 2001WO-US25840.	
XX		
PR	16-AUG-2000; 2000US-226326P.	
XX		
PA	(CHIR) CHIRON CORP.	
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F;	
PI	Lamson G, Scott EM, Zhang G, Kassam A, Pot D, Labat I;	
XX		
DR	WPI; 2002-241905/29.	
XX		
PT	New nucleic acid for producing a polypeptide, detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, and inhibiting tumor growth -	
PS	Claim 1; SEQ ID NO 3337; 883pp + Sequence Listing; English.	
XX		
CC	The invention relates to an isolated polynucleotide (ABN27253-ABN33262) with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as a probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therapeutic and diagnostic purposes. The polynucleotide is useful for gene therapy.	
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
XX		
SQ	Sequence 505 BP; 140 A; 130 C; 97 G; 138 T; 0 other;	
 Query Match		
	13.5%;	Score 27.8; DB 24; Length 505;

Best Local Similarity 57.5%; Pred. No. 22; Mismatches 50; Conservative 0; Gaps 0

Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0

QY 69 GAACAGGATAATAGAAGCAACGCCGATACAATTGGGTGGATTGGCAACAAACTCC 128
| | | | | | | | | | | | | | | | | | | | |
Db 338 GGACTAGGCAGGAAAAAATACTCAAGTGATGTCATTCTGGTTATATAGTAGCAGTAATGC 279
| | | | | | | | | | | | | | | | | | | | |

QY 129 TGTGACTAACAGGTCCTCATAGTTTTTCA 155
| | | | | | | | | | | | | | | | | | | | |
Db 278 TGTGAAGAACACAGGAAAATAGGTGTTTA 252
| | | | | | | | | | | | | | | | | | | | |

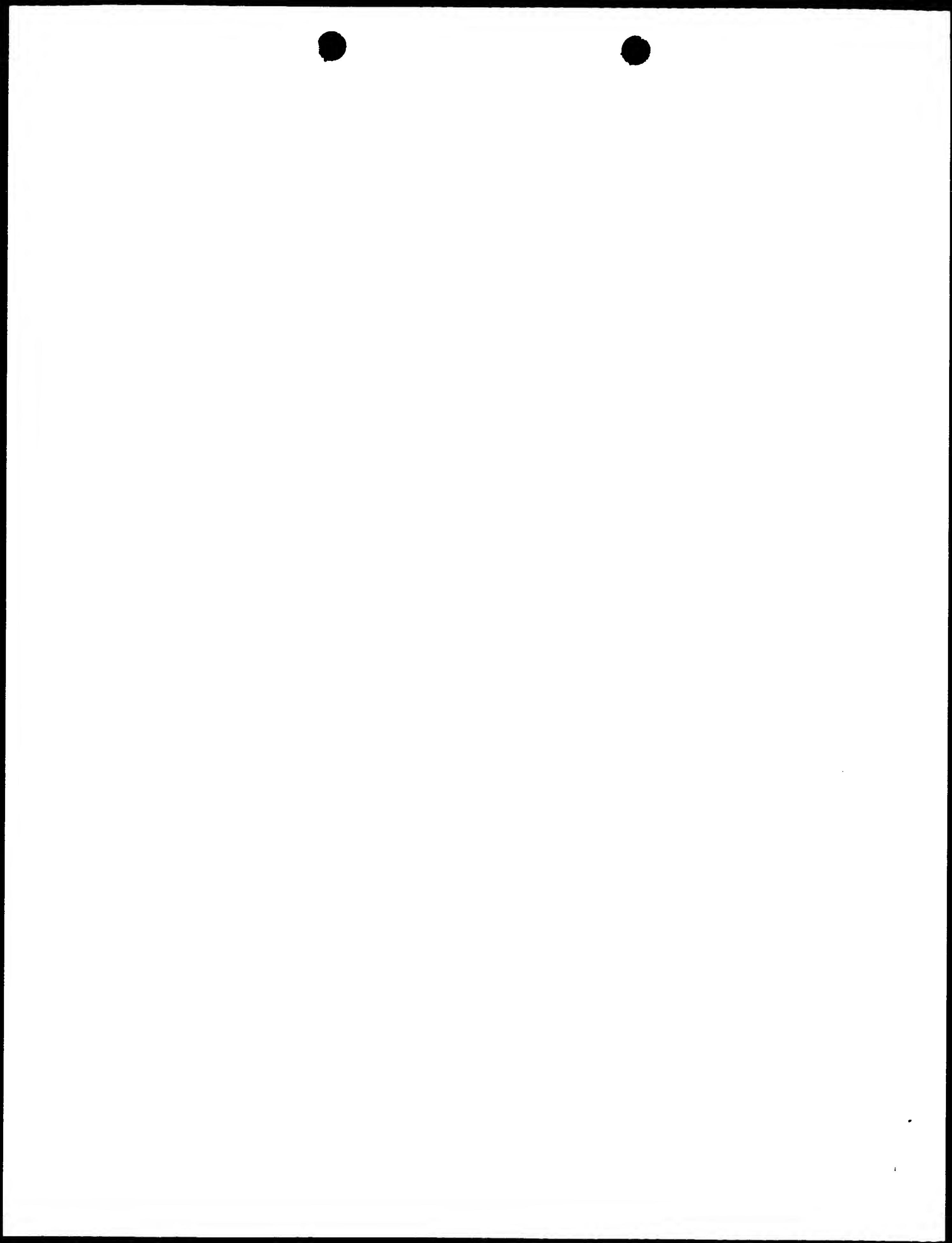
RESULT 74
AAS83874
ID AAS83874 standard; cDNA; 3019 BP.
XX
AC AAS83874;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19678.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG19687.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 19678; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AA94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 3019 BP; 958 A; 576 C; 649 G; 834 T; 2 other;

Db 2867 GCCTTAGAGTGG



GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 21:53:32 ; Search time 1184 Seconds
(without alignments)
2817.796 Million cell updates/sec

Title: 09-833799-13C
Perfect score: 206
Sequence: 1 gctcgagccatggtatggac.....gcaagggtgtattatcctag 206

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	38	18.4	604	17	AQ963597	AQ963597 LERGM96TF
C 2	37.6	18.3	603	17	AQ963598	AQ963598 LERGM96TF
3	35.4	17.2	852	17	CNS060DA	AL407924 T3 end of
C 4	34.8	16.9	721	17	AG012919	AG012919 Homo sapi
C 5	33.6	16.3	721	12	BF460287	BF460287 073H05 Ma
C 6	33.4	16.2	663	17	BH874885	BH874885 hg82c05.g

7	33.2	16.1	607	17	BH837348	BH837348
8	33.2	16.1	1292	13	BM458639	BM458639
C 9	33	16.0	298	12	BF818377	BF818377 CM1-CI003
10	33	16.0	1101	17	CNS00FS5	AL071181 Drosophil
C 11	32.6	15.8	450	10	AW026713	AW026713 vv4a10.x
C 12	32.6	15.8	467	9	AA760738	AA760738 nz10b01.s
C 13	32.6	15.8	607	10	AW031245	AW031245 EST274620
14	32.6	15.8	633	14	BQ413342	BQ413342 GA_Ed007
C 15	32.6	15.8	699	10	AW968686	AW968686 EST380762
16	32.6	15.8	1351	13	BM394905	BM394905 50072-2-6
17	32.4	15.7	502	14	BQ104605	BQ104605 fc1127.e
18	32.2	15.6	374	17	BH129215	BH129215 G-4m17.f
C 19	32	15.5	198	17	BH349323	BH349323 CH230-81C
20	32	15.5	865	17	AZ544449	AZ544449 ENTDY59TR
21	31.8	15.4	421	17	BH387315	BH387315 AG-ND-157
22	31.8	15.4	450	17	BH383717	BH383717 AG-ND-135
23	31.8	15.4	512	17	AQ933526	AQ933526 RPCI-23-2
24	31.8	15.4	617	17	CNS07GRE	AL610124 Anopheles
C 25	31.8	15.4	648	17	BH513269	BH513269 BOGLI44TR
C 26	31.8	15.4	684	17	BH521915	BH521915 BOGWO80TF
27	31.6	15.3	590	9	AL552214	AL552214 AL552214
C 28	31.6	15.3	653	17	AZ948884	AZ948884 2M0212B07
C 29	31.4	15.2	852	9	AU005855	AU005855 AU005855
30	31.2	15.1	471	13	BI808329	BI808329 C006H03 O
31	31.2	15.1	636	10	AW644945	AW644945 cm47C01.w
C 32	31.2	15.1	658	17	AZ858033	AZ858033 2M0163L02
C 33	31.2	15.1	801	17	BH381988	BH381988 AG-ND-172
C 34	31.2	15.1	872	17	AZ684794	AZ684794 ENTGK92TF
35	31.2	15.1	888	17	BH148262	BH148262 ENTPD89TR
C 36	31.2	15.1	956	14	BQ927018	BQ927018 AGENCOURT
37	31	15.0	580	17	AQ078766	AQ078766 CIT-HSP-2
38	31	15.0	608	17	AQ257960	AQ257960 nbxb0019B
39	31	15.0	873	17	BH461787	BH461787 BOGTD72TR
40	31	15.0	1996	9	AL697315	AL697315 AL697315
41	30.8	15.0	427	10	AW024040	AW024040 df64f12.y
C 42	30.8	15.0	581	13	BI405270	BI405270 UMN52B09
43	30.6	14.9	416	17	FR0022243	AL015113 F.rubripe
44	30.6	14.9	458	10	AW264970	AW264970 xq58f08.x
C 45	30.6	14.9	539	17	AZ900700	AZ900700 RPCI-24-1
C 46	30.6	14.9	720	14	BQ514381	BQ514381 EST621796
C 47	30.6	14.9	862	12	BF185163	BF185163 601843828
48	30.2	14.7	304	14	N65641	N65641 20681 Lambd
49	30.2	14.7	390	10	AV427714	AV427714 AV427714
50	30.2	14.7	554	17	BH408584	BH408584 1007005B1
51	30.2	14.7	566	17	BH408577	BH408577 1007005A1
C 52	30.2	14.7	582	10	BE604036	BE604036 GS419-T7
C 53	30.2	14.7	629	17	AQ932853	AQ932853 RPCI-23-2
54	30	14.6	476	17	AQ757100	AQ757100 HS_5448.B
C 55	30	14.6	513	14	BQ637372	BQ637372 he09c01.y
C 56	30	14.6	519	12	BG384279	BG384279 303302 MA
57	30	14.6	631	17	BH305658	BH305658 CH230-179
58	30	14.6	697	17	BH200757	BH200757 Sm1-45O18
C 59	29.8	14.5	313	14	BQ250036	BQ250036 Tae25010F
C 60	29.8	14.5	400	12	BG406256	BG406256 sac29e02.
61	29.8	14.5	423	13	BM433714	BM433714 10M03H09
62	29.8	14.5	539	9	AI975607	AI975607 EST270201
63	29.8	14.5	581	10	AV617820	AV617820 AV617820
C 64	29.8	14.5	587	12	BF009213	BF009213 ss75e02.y
65	29.8	14.5	593	12	BF042233	BF042233 BP250021B
66	29.8	14.5	637	9	AI976453	AI976453 EST271047
67	29.8	14.5	638	13	BI421295	BI421295 EST531961
68	29.8	14.5	664	12	BF046370	BF046370 BP250021A
69	29.8	14.5	712	12	BF936455	BF936455 EST459510
70	29.8	14.5	944	17	AZ668876	AZ668876 ENTJR88TR
C 71	29.8	14.5	1002	14	BQ064772	BQ064772 AGENCOURT
C 72	29.6	14.4	424	17	BH633508	BH633508 SALK_0426
C 73	29.6	14.4	454	17	BH633544	BH633544 SALK_0427
74	29.6	14.4	474	13	BI004390	BI004390 MR4-HN005
C 75	29.6	14.4	498	12	BF731738	BF731738 3092-33 h
C 76	29.6	14.4	536	10	AV529350	AV529350 AV529350
77	29.6	14.4	551	13	BM426131	BM426131 pgf2n.pk0
C 78	29.6	14.4	568	13	BG915672	BG915672 602814164
C 79	29.6	14.4	586	9	AU209278	AU209278 AU209278


```

Saccharomyces exiguus, genomic survey sequence.
ACCESSION      AL407924
VERSION        AL407924.1  GI:12174045
KEYWORDS       GSS.
SOURCE         Saccharomyces exiguus.
ORGANISM       Saccharomyces exiguus
               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
               Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE      1 (bases 1 to 852)
AUTHORS        Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
               Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
               de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
               Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
               Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
               Wincker,P. and Weissenbach,J.
TITLE          Genomic exploration of the hemiascomycetous yeasts: 1. A set of
               yeast species for molecular evolution studies
JOURNAL        FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE        20584711
PUBMED        11152876
REFERENCE      2 (bases 1 to 852)
AUTHORS        Bon,E., Neuveglise,C., Lepingle,A., Wincker,P., Artiguenave,F.,
               Gaillardin,C. and Casaregola,S.
TITLE          Genomic exploration of the hemiascomycetous yeasts: 6.
               Saccharomyces exiguus
JOURNAL        FEBS Lett. 487 (1), 42-46 (2000)
MEDLINE        20584716
PUBMED        11152881
REFERENCE      3 (bases 1 to 852)
AUTHORS        Direct Submission
TITLE          Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
               2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
               seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL        This GSS is part of a random genomic sequencing program of thirteen
               yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
               exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
               Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
               lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
               angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
               Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
               5 kb were prepared and both extremities were sequenced. See
               keywords for description of this sequence and for the sequence of
               the other extremity of this insert.
FEATURES       Location/Qualifiers
               1..852
               /organism="Saccharomyces exiguus"
               /strain="CBS 379"
               /db_xref="taxon:34358"
               /clone="AV0AA005E04"
               /clone_lib="AV0AA"
               /note="end : T3"
               misc_feature
               <2..>445
               /note="similar to Saccharomyces cerevisiae ORF YBR068c [
               BAP2 ; leucine permease, high-affinity (S1) ]
               similar to Saccharomyces cerevisiae ORF YDR046c [ BAP3 ;
               valine transporter ]"
               /evidence=not_experimental
BASE COUNT     275 a 143 c 129 g 303 t 2 others
ORIGIN
Query Match    17.2%; Score 35.4; DB 17; Length 852;
Best Local Similarity 57.8%; Pred. No. 2;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 49 ACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGGCATACAATTGGG 108
|||||
Db 727 ACACAGTTTATTGAATCTTAAATAAACTTATATAAGTAACCAACGTGACATTTTCCATA 786
|||||

QY 109 TGGATTGGCAACAACCTCCTGTGACTAACAGGTCCATAGTTTTTTCACG 157
|||||
Db 787 AGGATTGAGATCAATCTTTTTTTGTCTCTCATTTCTCTCATTTTTCATG 835
|||||
```

```

RESULT 4
AG012919/c
LOCUS          AG012919
DEFINITION     Homo sapiens genomic DNA, 21q region, clone: f1E12X11, genomic
               survey sequence.
ACCESSION      AG012919
VERSION        AG012919.1  GI:3450813
KEYWORDS       GSS.
SOURCE         Homo sapiens DNA, clone:f1E12X11.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 721)
AUTHORS        Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE          Homo sapiens genomic DNA, chromosome 21q
JOURNAL        Published Only in DataBase (1998)
REFERENCE      2 (bases 1 to 721)
AUTHORS        Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE          Direct Submission
JOURNAL        Submitted (23-AUG-1998) Masahira Hattori, Kitasato University,
               Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
               Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
               Tel:0427-78-9732, Fax:0427-78-9561)
FEATURES       Location/Qualifiers
               1..721
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /chromosome="21"
               /map="21q"
               /clone="f1E12X11"
BASE COUNT     142 a 173 c 148 g 149 t 109 others
ORIGIN
Query Match    16.9%; Score 34.8; DB 17; Length 721;
Best Local Similarity 54.8%; Pred. No. 2.8;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 45 CAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGGCATACAATT 104
|||||
Db 213 CAAGAAAAACAACCTTCTGTCAAAGATCAGTAAACCGAGACTCATCAACAGATCCAAGT 154
|||||

QY 105 TGGGTGGATTGGCAACAACCTTCTGTGACTAACAGGTCCATAGTTTTTTCAGCACACTTC 164
|||||
Db 153 TGCAAGCCTTTTCAAAATTTTACAAAGGAATCAGTTTCCAAAGATTTCCCCCATATTTC 94
|||||

QY 165 CAAGGA 170
|||||
Db 93 CAAGAA 88

RESULT 5
BF460287/c
LOCUS          BF460287
DEFINITION     073H05 Mature tuber lambda ZAP Solanum tuberosum cDNA 5', mRNA
               sequence.
ACCESSION      BF460287
VERSION        BF460287.1  GI:11529444
KEYWORDS       EST.
SOURCE         potato.
ORGANISM       Solanum tuberosum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE      1 (bases 1 to 721)
AUTHORS        Nielsen,K.L., Crookshanks,M., Emmersen,J. and Welinder,K.G.
TITLE          EST-sequencing of mature potato tuber (Var. Kuras)
JOURNAL        Unpublished (2000)
COMMENT        Contact: Karen G. Welinder
               Institut for bioteknologi
               Aalborg Universitet
               Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
               Tel: +45 96358467
```

Fax: +45 98141808
Email: kgw@bio.auc.dk
High quality sequence stop: 721
POLYA=No.

FEATURES

source

Location/Qualifiers
1. .721
/organism="Solanum tuberosum"
/cultivar="Field grown Kuras"
/db_xref="taxon:4113"
/clone_lib="Mature tuber lambda ZAP"
/tissue_type="Tuber"
/note="Vector: Lambda ZAP"

208 a 173 c 112 g 228 t

BASE COUNT
ORIGIN

Query Match 16.3%; Score 33.6; DB 12; Length 721;
Best Local Similarity 52.1%; Pred. No. 6.9;
Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 17 GGACGTATACGAGTCTCTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGA 76

Db 176 GGAGAACATCAGTTGCCAGGAAATTTTCAGTAGTGTCAATGCATACGGAACAGGA 117

QY 77 TAATAGAACTAAGCAACGGCATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTA 136

Db 116 TGAACCTCATGCTCCATGGGAAAGAATTCAGTAGAATTTGAGAGAAAGGAGTGTGACTT 57

QY 137 ACAGTCCATAGTTTTTTCACGACA 160

Db 56 ACAGAACTCCAATTTTGAACCA 33

RESULT 6

BH874885/c

LOCUS BH874885 663 bp DNA linear GSS 05-AUG-2002
DEFINITION hg82c05.g1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays genomic clone hg82c05 5', DNA sequence.

ACCESSION

BH874885

VERSION BH874885.1 GI:22110782

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 663)

Rabinowicz,P.D., O'Shaughnessy,A.L., Balijs,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zutavern,T., McCombie,W.R. and Martienssen,R.A.

Genomic shotgun sequences from Zea mays (methyl-filtered)

Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: hg82 row: c column: 05

Seq primer: -21M13UnivFwd

Class: shotgun

High quality sequence stop: 663.

Location/Qualifiers

1. .663

/organism="Zea mays"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="hg82c05"

/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"

/lab_host="JM107 or DH5a"

/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;

The vector was digested with XbaI and one nucleotide was

added by fill in in the recessive 3' end. The genomic DNA

was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "

BASE COUNT 168 a 139 c 125 g 231 t

ORIGIN

Query Match 16.2%; Score 33.4; DB 17; Length 663;

Best Local Similarity 60.4%; Pred. No. 7.6;

Matches 55; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 51 ACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTG 110

Db 132 ACACCATATTATCTACATCAATGTTTACTGGAATAAAGATGAGAGAAGCATTTTGGGTG 73

QY 111 GATTGGCAACAACTTCCTGTGACTAACAGG 141

Db 72 TATAGGTGACAAACATAATGCAACAATCAGG 42

RESULT 7

BH837348

LOCUS

DEFINITION

BH837348 607 bp DNA linear GSS 28-MAY-2002

Locus LMCRO50012H06f Zea mays L. Zea mays genomic clone LMCRO50012H06f, DNA sequence.

ACCESSION

BH837348

VERSION BH837348.1 GI:21235226

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 607)

Kim,S.W., Yu,Y., Lee,M.C., Main,D. and Wing,R.A.

Methyl-filtration genomic sequence from maize

Unpublished (2002)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total High Quality bases = 546

Seq primer: TAATACGACTCACTATAGG

Class: shotgun

High quality sequence start: 2

High quality sequence stop: 598.

Location/Qualifiers

1. .607

/organism="Zea mays"

/strain="B73"

/db_xref="taxon:4577"

/clone="LMCRO50012H06f"

/clone_lib="Zea mays L."

/tissue_type="Leaf"

/lab_host="DH10B"

/note="Vector: pGEM-T easy; Site 1: Mcr BC;

Methyl-filtration library, Nuclei DNA was completely

digested with Mcr BC, size fractionated and transformed

to E.Coli.DH10B."

BASE COUNT 178 a 130 c 124 g 174 t 1 others

ORIGIN

Query Match 16.1%; Score 33.2; DB 17; Length 607;

Best Local Similarity 57.8%; Pred. No. 8.5;

Matches 59; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 40 ATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAGCAACGCGATA 99

Db 263 AATTCAACATTACACCACCATTTATCTACAATCAATGTTTACTGGAATAAAGATGAGAGAAG 322

QY 100 CAATTTGGTGGATTGGCAACAACAACTTCTCTGACTAACAGG 141
|||||
Db 323 CATTTTGGGTATAGGTGACAAACATAATGCAACAATCAAG 364
|||||

RESULT 8
BM458639
LOCUS
DEFINITION
AGENCOURT_6413495 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5497704
5', mRNA sequence.

ACCESSION
BM458639
VERSION
BM458639.1 GI:18507679
KEYWORDS
EST.
SOURCE
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1292)

REFERENCE
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12128 row: e column: 01
High quality sequence stop: 224.

FEATURES
source
1..1292
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5497704"
/clone_lib="NIH_MGC_85"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 346 a 355 c 264 g 320 t 7 others
ORIGIN

Query Match 16.1%; Score 33.2; DB 13; Length 1292;
Best Local Similarity 54.0%; Pred. NO. 12;
Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 71 ACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAACTTCCTG 130
|||||
Db 252 ACAGGTGATCTGGACCAAGATGGGAGGATCAGTTTGTGATGAATTTATTACAGATTTCCTT 311
|||||

QY 131 TGACTAACAGGTCCATAGTTTTCACGACACITTCGAAGGACGCCATACCGAACAAGCAA 190
|||||
Db 312 GGCCTAAAAGCCACAATGTTGCCAGACCITTTAAAAAACCCACTCATAACAAGGAA 371
|||||

QY 191 GGTGTT 196
|||||
Db 372 GGGATT 377
|||||

RESULT 9
BF818377/c
LOCUS
DEFINITION
CM1-CI0032-191200-630-c11 CI0032 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF818377
VERSION
BF818377.1 GI:12155643
KEYWORDS
EST.

SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 298)

REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1&t2=CM1-CI0032-
191200-630-c11&t3=2000-12-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 298.
High quality Location/Qualifiers
1..298
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CI0032"
/dev_stage="Adult"
/note="Organ: colon ins; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 63 a 80 c 76 g 79 t
ORIGIN

Query Match 16.0%; Score 33; DB 12; Length 298;
Best Local Similarity 51.0%; Pred. NO. 7;
Matches 78; Conservative 0; Mismatches 75; Indels 0; Gaps 0

QY 6 AGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
|||||
Db 200 ATCTCTGCTAGAGGCTGGCGTCTTCTCCGAGCATGTGGGGAGCCAGATGGGTCTTG 141
|||||

QY 66 CAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAACT 125
|||||
Db 140 TTCTTTGGGATGTGGGAACCTAAGCCATGAGACAAGTTAAGGCGATGTCGAGAACAAACT 81
|||||

QY 126 TCCTGTGACTAACAGGTCCATAGTTTTTTCACGA 158
|||||
Db 80 CTCAGAAATGGCTTTTAGGAGTTTTTACTGA 48
|||||

RESULT 10
CNS00FS5
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR31K23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL071181
VERSION
AL071181.1 GI:4951021
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster.

Db 192 AGTTCATTNTTCATTTCCAGGACAAAAATGAATCGTTAAGAACACAGATTAAAGAAAATTA 251

Qy 88 AGCA 91
| | |

Db 252 AACA 255

RESULT 15
AW968686/c
LOCUS AW968686 699 bp mRNA linear EST 01-JUN-2000
DEFINITION EST380762 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
ACCESSION AW968686
VERSION AW968686.1 GI:8158527
KEYWORDS EST.
SOURCE human

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 699)

REFERENCE

AUTHORS

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.

TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)

COMMENT

Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

```

FEATURES
source
1. .699
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGJ"
/note="Vector: pBluescriptSKm"
226 a 142 c 107 g 224 t
BASE COUNT

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Query Match      15.8%; Score 32.6; DB 10; Length 699;
Best Local Similarity 57.3%; Pred. No. 14;
Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY   19 ACGTATACGAGTTCCTTGTTCAATTCCAGGCACACAGATGATTCGGTCCAAGAACAAGGATA 78
     ||||| |||||| | | | | | | | | | | | | | | | |
Db    430 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGGTAA 371

QY   79 ATAGAACTAAGCAAACGCCGATACAAATTGGGTGGATTGGCAACA 121
     || | | | | | | | | | | | | | | | |
Db    370 GTGCAGGAAAACAAGAGAAATATTTTCAGAGTATAGTCAAAA 328


RESULT 16
BM394905
LOCUS       BM394905                1351 bp          mRNA
DEFINITION  50072-2-6-F01.r.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila CDNA, mRNA sequence.
```

Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES	source
1..1351	Location/Qualifiers
/organism="Tetrahymena thermophila"	
/strain="CU428.1"	
/db_xref="taxon:5911"	
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"	
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci. USA. 98: 8709-8713."	

BASE COUNT	387 a	325 c	324 g	306 t	9 others
ORIGIN					

Query Match 15.8%; Score 32.6; DB 13; Length 1351;
Best Local Similarity 49.1%; Pred. No. 19;
Matches 86; Conservative 0; Mismatches 89; Indels 0;

QY	31	TCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAAGC	90
Db	730	TATTAGCCAAAAACAGGCGCGCAGGAGGGGTTAAACCCACGGCGAATCGGAAGGGGC	789
QY	91	AACGGGATACAAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCTATAGTT	150
Db	790	GACAACATATAAGCGGGCGAACGGAAATGACACCTATAGAGAGAGACTCCGACTTCTT	849
QY	151	TTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTATCCTA	205
Db	850	TCTCACGACAGATCTTATGTGCGATATACCTACGATTCGACCGAGAGGTTGAATCTA	904

RESULT 17
BQ104605
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 502)

AUTHORS	Menda, N., Guterman, I., Piestun, D., Emanuel, M., Adam, Z., E., Lewinsohn, E., Zamir, D., Vainstein, A. and Weiss, D.
TITLE	Rose petal genomics: an integrated approach to discover fragrance-related genes
JOURNAL	Unpublished (2002)
COMMENT	Contact: Naama Menda

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI069YA02"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 165 a 129 c 37 g 205 t 54 others
ORIGIN

Query Match 15.3%; Score 31.6; DB 9; Length 590;
Best Local Similarity 54.2%; Pred. No. 27;
Matches 52; Conservative 5; Mismatches 39; Indels 0; Gaps 0;

QY 76 ATAATAGAACTAAGCAACGCGATACAAATTGGGTGGATTGGCAACAACTTCTGTGACT 135
|||||
Db 36 ATCATTTTATTAATAAATAATATTCAATTCATTTTAATKKKTAATAAACTTATAATTCAT 95
|||||

QY 136 AACAGGTCCATAGTTTTCACGACACTTCCCAAGGAC 171
|||||
Db 96 AACTACTCCAAGATKTTCAKKAACCAACCAAAAGAC 131
|||||

RESULT 28
AZ948884/c
LOCUS 2M0212B07F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0212B07 F, DNA sequence.
ACCESSION AZ948884
VERSION AZ948884.1 GI:13820111
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 653)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: B column: 07
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 653.

FEATURES
source
1. .653
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0212B07"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 157 a 128 c 117 g 251 t
ORIGIN

Query Match 15.3%; Score 31.6; DB 17; Length 653;
Best Local Similarity 55.5%; Pred. No. 29;
Matches 61; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 17 GGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGA 76
|||||
Db 600 GGACATACTCTTAAATAGGTATATTTAAGACACCAAGTAATCTTTACAAATACAGGA 541
|||||

QY 77 TAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTT 126
|||||
Db 540 AAATTAAGTAACCTTACTCTATCCAATCTGATTAATAATGGAATTAAGTT 491
|||||

RESULT 29
AU005855/c
LOCUS AU005855 Bombyx mori p50(Daizo) Bombyx mori cDNA clone wv40184,
DEFINITION mRNA sequence.
ACCESSION AU005855
VERSION AU005855.1 GI:4163239
KEYWORDS EST.
SOURCE domestic silkworm.
ORGANISM Bombyx mori

REFERENCE 1 (bases 1 to 852)
AUTHORS Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
TITLE Establishment of cDNA database of Bombyx mori
JOURNAL Unpublished (1999)
COMMENT Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
PROJECT = 'CREST project by JST'.
Location/Qualifiers

FEATURES
source
1. .852
/organism="Bombyx mori"
/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="wv40184"
/clone_lib="Bombyx mori p50(Daizo)"
BASE COUNT 269 a 138 c 155 g 290 t
ORIGIN

Query Match 15.2%; Score 31.4; DB 9; Length 852;
Best Local Similarity 51.0%; Pred. No. 38;
Matches 74; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 49 ACACAGATGATTCGGTCCAAAGACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGG 108

```

Db      723 ACACAGTAGGTATGGATTTACCACATATCTTTGAGAGCCCAAGGAAGTCTCTCAACATAGGCT 664
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      109 TGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTCACGACACATTCCTCAAG 168
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      663 TATAGTTCGAAGAACCTTGTGTGAGAGTGAACTGAGTCTAATCTTCCACAACATTAGCAAC 604
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      169 GACGCCATACCGAACAAAGCAAGGT 193
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      603 TGCATCAAGCGCATCAGAAAAAGAT 579
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 30
BI808329
LOCUS
DEFINITION
  BI808329 471 bp mRNA linear EST 02-OCT-2001
  C006H03 Oryza sativa mature leaf library induced by M.grisea Oryza
  sativa cDNA clone C006H03, mRNA sequence.
ACCESSION
  BI808329
VERSION
  BI808329.1 GI:15855517
KEYWORDS
  EST.
SOURCE
  Oryza sativa.
  Oryza sativa
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzeae; Oryza.
  1 (bases 1 to 471)
AUTHORS
  Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
  ,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE
  A Gene Expression Screen in Oryza sativa
JOURNAL
  Unpublished (2001)
COMMENT
  Contact: Dong HT
  Laboratory of Functional Genetics
  Bio-technology Institute of Zhejiang University
  Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
  Tel: 0086-571-86892051
  Fax: 0086-571-86961525
  Email: htdong@zjuem.zju.edu.cn
  Seq primer: M13 forward primer.
  Location/Qualifiers
    1..471
      /organism="Oryza sativa"
      /db_xref="taxon:4530"
      /clone="C006H03"
      /clone_lib="Oryza sativa mature leaf library induced by
      M.grisea"
      /tissue_type="leaf"
      /dev_stage="Mature stage"
      /note="Vector: pSport2"
BASE COUNT 137 a 102 c 105 g 127 t
ORIGIN

Query Match 15.1%; Score 31.2; DB 13; Length 471;
Best Local Similarity 54.3%; Pred. No. 33;
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY      75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      350 GATATAAAACATACACTTCAGCATATTATTATTGTATATAGTCATCAAACTTGTGTTGAC 409
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      135 TAACAGGTCCATAGTTTTCACGACACTTCCCAAGGAGCGCCATACCGAACAAAGCAA 190
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      410 TACTTTGCCTGCAGTATATCTCATAAACCAAGAAGATTGGATAGAAAAA 465
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 31
AW644945
LOCUS
DEFINITION
  AW644945 636 bp mRNA linear EST 26-APR-2001
  cm47c01.w1 Blackshear/Soares normalized Xenopus egg library Xenopus
  laevis cDNA clone PBX0146C01 5', mRNA sequence.
ACCESSION
  AW644945
VERSION
  AW644945.1 GI:7402350
KEYWORDS
  EST.
SOURCE
  African clawed frog.

```


LOCUS AZ858033 658 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0163L02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0163L02 F, DNA sequence.
ACCESSION AZ858033
VERSION AZ858033.1 GI:13050772
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 658)
AUTHORS Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: L column: 02
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 658.

FEATURES source
1..658
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163L02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 178 a 128 c 152 g 200 t
ORIGIN
Query Match 15.1%; Score 31.2; DB 17; Length 658;
Best Local Similarity 52.3%; Pred. No. 39;
Matches 69; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 73 AGGATAATAGAACTAAGCAACGGATACAATTTGGTGGATTGGCAACAACCTTCCTGTG 132
|||||
Db 297 AGGAAGTTGAAGTTGGCCTCACTAATTTACATAGTGGCTTAGACAAACTCTTCAACTT 238
QY 133 ACTAACAGGTCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAAGCAAGG 192
|||||
Db 237 TCCAGCTTCCCGCAACTGTACTCATCATCAGCTACAAGTTCCTTACCCCAACAAAGAGTGG 178

QY 193 TGTATTATTACCT 204
|||||
Db 177 TTTTAATGCCTT 166
RESULT 33
BH381988/c
LOCUS BH381988 801 bp DNA linear GSS 10-DEC-2001
DEFINITION AG-ND-172E18.TR ND-TAM Anopheles gambiae genomic clone AG-ND-172E18, DNA sequence.
ACCESSION BH381988
VERSION BH381988.1 GI:17328130
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE 1 (bases 1 to 801)
AUTHORS Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other GSSs: AG-ND-172E18.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
Seq primer: M13 Rev
Class: BAC ends.

FEATURES source
1..801
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-172E18"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site 1: HindIII"

BASE COUNT 148 a 216 c 157 g 280 t
ORIGIN
Query Match 15.1%; Score 31.2; DB 17; Length 801;
Best Local Similarity 56.2%; Pred. No. 43;
Matches 45; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 66 CAAGAACAGGATAATAGAACTAAGCAACGGATACAATTTGGTGGATTGGCAACAACACT 125
|||||
Db 395 CAAGAAAAAATAAGTAAGTAAGTCCCAAGGAAGCATTAAGGTGAGTCCGAAGAAGGT 336
QY 126 TCCTGTGA 133
|||||
Db 335 TCCTGTGA 328

RESULT 34
AZ684794/c
LOCUS AZ684794 872 bp DNA linear GSS 14-DEC-2000
DEFINITION ENTGK92TF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.
ACCESSION AZ684794
VERSION AZ684794.1 GI:11821940

Seq primer: M13-21
Class: BAC ends.

```

/contype= pfam
/note="Vector: pBeloBAC11;
HindIII"

```

HindIII"

Query Match 15.0%: Score 31: DB

RESULT 38

AQ257560
LOCUS
AQ257960
608 bp
D

RECESSION
VERSION
A0257960.1
GI:3782442

ORGANISM *Coryza pacifica*
Eukaryota: Viridiplantae: Streptophyta

AUTHORS Wang, K.A. and Dean, K.A.

TITLE A BAC End Sequencing Framework to Sequence

Clemson University
100 Jordan Hall, Clemson, SC 29634.

Email: lw1ng@cremson.edu
Seq primer: GGAAACAGCTATGACCATG

```
/scans= japonica
/cultivar="Nipponbare"
```

```

/issue_type="Deal"
/lab_host="E_coli_DH10B"

```

immigrating highly polarized populations, rely on rich and subtropical, rely on rich

(Arumuganathan and Earle, 1985).

AW024040
LOCUS AW024040 427 bp mRNA linear EST 12-NOV-1999
DEFINITION df64f12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:2488487 5', mRNA sequence.
ACCESSION AW024040
VERSION AW024040.1 GI:58777570
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 427)
AUTHORS Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R.
and Morton, C.C.
TITLE Isolation of novel and known genes from a human fetal cochlear cDNA
library using subtractive hybridization and differential screening
JOURNAL Genomics 23, 42-50 (1994)
MEDLINE 95130111
COMMENT Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and
Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996
Email: cmorton@bics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLAM6191 row: L column: 24
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
FEATURES
source
1..427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2488487"
/clone_lib="Morton Fetal Cochlea"
/tissue_type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
XR Vector. Library constructed by N. Robertson, C. Morton.
~5' adaptor sequence: 5' GAATTCGGCAGG 3' ~3' adaptor
sequence: 5' CTCAGTGTCTTTTCTTTT 3"
BASE COUNT 139 a 57 c 94 g 137 t
ORIGIN
Query Match 15.0%; Score 30.8; DB 10; Length 427;
Best Local Similarity 54.4%; Pred. No. 42;
Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 19 ACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGACAGGATA 78
Db 302 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGGTAA 361
QY 79 ATAGAACTAAGCAACGCCGATACAAATTTGGGTGGATTGGCAACAACTTCCTGTG 132
Db 362 GTCAGGAAACAAGAGAAATATTTTCAGAGTATAAGTCAAAAGTACACTGAG 415
RESULT 42
BI405270/c
LOCUS BI405270 581 bp mRNA linear EST 14-AUG-2001
DEFINITION UMN52B09 Canine Brain cDNA Library Canis familiaris cDNA 5', mRNA
sequence.
ACCESSION BI405270
VERSION BI405270.1 GI:15184483
KEYWORDS EST.

SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 581)
AUTHORS Roberts, M.C., Hendrickson, J.A., Hoffmann, D.E., Flickinger, G.H.,
Rutherford, M.S., and Mickelson, J.R.
TITLE University of Minnesota Canine Brain EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Mickelson, J.R.
Veterinary Pathobiology
University of Minnesota
1988 Fitch Avenue, University of Minnesota, St. Paul, MN 55108, USA
Tel: 612 624 1246
Fax: 612 625 0204
Email: micke001@umn.edu
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source
1..581
/organism="Canis familiaris"
/db_xref="taxon:9615"
/clone_lib="Canine Brain cDNA Library"
/sex="Male"
/note="Organ: Brain; Vector: pSPORT1 (Gibco BRL); Site_1:
NotI; Site 2: SalI; Tissue was taken from the frontal,
occipital, temporal and parietal lobes, olfactory bulb,
hippocampus, cerebellum, thalamus, hypothalamus, midbrain
, pons, and medulla."
BASE COUNT 96 a 186 c 172 g 117 t 10 others
ORIGIN
Query Match 15.0%; Score 30.8; DB 13; Length 581;
Best Local Similarity 58.8%; Pred. No. 49;
Matches 50; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 21 GTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGACAGGATAAT 80
Db 473 GTATCCAAGTTCCTGATGGAATTCGGTTCACAGAACACTCGATACAGCATTTNGCAA 414
QY 81 AGAACTAAGCAACGCCGATACAAATTT 105
Db 413 CNCTTAAGCCACCCCGTTATNAGTT 389
RESULT 43
FR0022243
LOCUS FR0022243 416 bp DNA linear GSS 10-DEC-1997
DEFINITION F.rubripes GSS sequence, clone 074I20af3, genomic survey sequence.
ACCESSION AL015113
VERSION AL015113.1 GI:2681481
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes.
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
REFERENCE 1 (bases 1 to 416)
AUTHORS Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrana, Y.,
Williams, G. and Brenner, S.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
Centre Hinxtan, Cambridge, CB10 1SB. Email: biohelp@hgmrc.ac.uk
COMMENT Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
Location/Qualifiers
FEATURES
source
1..416
/organism="Takifugu rubripes"
/db_xref="taxon:31033"

ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 720)
AUTHORS Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karamycheva,S.A.
TITLE Generation of a set of potato cDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT Other_ESTs: EST621795
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@tigr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdna@resgen.com
Seq primer: T7.

FEATURES Location/Qualifiers
1..720
/organism="Solanum tuberosum"
/cultivar="Kennebec Or Binjte"
/db_xref="taxon:4113"
/clone="STM158"
/clone_lib="Generation of a set of potato cDNA clones for
microarray analyses mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
, tubers, or roots."
BASE COUNT 203 a 164 c 145 g 208 t
ORIGIN
Query Match 14.9%; Score 30.6; DB 14; Length 720;
Best Local Similarity 56.4%; Pred. No. 63;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 28 AGTCTTGGTCAATTTCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTA 87
Db 618 AGCTCTAGGGCTACTTCGAGGGTCCATAGTAGGGATGAGTTGACAGAAAAGAGAAGCA 559
QY 88 AGCAACGGCATACAATTGGGTGGATTGGCAACAACACTTC 128
Db 558 AGCATTCGGAGAGAACTTTTACTGACTTGGCATCATGTCGTAC 518

RESULT 47
BF185163/c
LOCUS BF185163 862 bp mRNA linear EST 31-OCT-2000
DEFINITION 601843828F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064670 5',
mRNA sequence.
ACCESSION BF185163
VERSION BF185163.1 GI:11063592
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 862)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM899 row: g column: 07
High quality sequence stop: 596.
FEATURES Location/Qualifiers
1..862
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4064670"
/clone_lib="NIH_MGC_54"
/tissue_type="from Chronic myelogenous leukemia"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCGGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 244 a 137 c 180 g 301 t
ORIGIN

Query Match 14.9%; Score 30.6; DB 12; Length 862;
Best Local Similarity 51.9%; Pred. No. 69;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 67 AAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAACTT 126
Db 708 AACAAATTGGAAAAGAAATACGTTTCAGCTTAGTTTCATTTTCGGTCTCTTCCAAAAATGTA 649
QY 127 CCTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAAGGACGCCATACCGAACAAA 186
Db 648 CTGTCTACCAACCTCGACCATATAAGAGACATTTTCAAAACCACCAACCCAGAAAAG 589
QY 187 GCAAGGTGTTATT 199
Db 588 AACAGGTATCATT 576

RESULT 48
N65641
LOCUS N65641 304 bp mRNA linear EST 05-JAN-1998
DEFINITION 20681 Lambda-PRL2 Arabidopsis thaliana cDNA clone 240K9T7, mRNA
sequence.
ACCESSION N65641
VERSION N65641.1 GI:1217267
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 304)
AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
,E. and Somerville,C.
TITLE Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
JOURNAL 95148729
MEDLINE
COMMENT Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.

[illegible]

[illegible]

Qy 169 GACGCCATACCGAAC 183
|||
Db 338 AACTCAAAATAGAGC 324

```

RESULT 54
AQ757100
LOCUS
DEFINITION
  AQ757100 476 bp DNA linear GSS 27-JUL-1999
  HS_5448_B2_E12_T7A_RPCI-11 Human Male BAC Library Homo sapiens
  genomic clone Plate=1024 Col=24 Row=J, DNA sequence.
ACCESSION
  AQ757100
VERSION
  AQ757100.1 GI:5621903
KEYWORDS
  GSS.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 476)
  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
  Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
  Hood,L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  99380589
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Clones are derived from the human BAC library RPCI-11. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
  or from Resear h Genetics (info@resgen.com). BAC end web Server:
  http://www.htsc.washington.edu
  Plate: 1024 row: J column: 24
  Seq primer: T7
  Class: BAC ends
  High quality sequence stop: 476.
FEATURES
  source
    1..476
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="Plate=1024 Col=24 Row=J"
    /clone_lib="RPCI-11 Human Male BAC Library"
    /sex="male"
    /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
    Male blood DNA was isolated from one randomly chosen donor
    and partially digested with a combination of EcoRI and
    EcoRI Methylase. Size selected DNA was cloned into the
    pBACe3.6 vector at EcoRI sites"
BASE COUNT
  163 a 84 c 85 g 138 t 6 others
ORIGIN
  Query Match 14.6%; Score 30; DB 17; Length 476;
  Best Local Similarity 60.8%; Pred. No. 80;
  Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

  QY 9 CATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68
    |||||
  Db 5 CAGGGTTTGGAGCTTGAGGCCCTCCTGGAGACCCCTCGANCAACNCAATTGGAGACGGTCCAA 64
    |||||

  QY 69 GAACAGGATAATAG 82
    |||||
  Db 65 GNACAGATAAGNG 78

RESULT 55
BQ637372/c
LOCUS
DEFINITION
  BQ637372 513 bp mRNA linear EST 15-JUL-2002
  he09c01.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
  Homo sapiens cDNA clone he09c01 5', mRNA sequence.
ACCESSION
  BQ637372
VERSION
  BQ637372.1 GI:21761831
KEYWORDS
  EST.

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RESULT 53
AQ932853/c
LOCUS      629 bp    DNA        linear   GSS 21-DEC-1999
DEFINITION RPCI-23-268D24.TJ RPCI-23 Mus musculus genomic clone RPCI-23-268D24
            , DNA sequence.
ACCESSION  AQ932853
VERSION    AQ932853.1  GI:6621959
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 629)
AUTHORS    Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
TITLE      Mouse BAC End Sequences from Library RPCI-23
JOURNAL
COMMENT    Other_GSSs: RPCI-23-268D24.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tldb/bac\_ends/mouse/bac\_end\_intro.html
            Plate: 268 row: D column: 24
            Seq primer: SP6
            Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..629
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-268D24"
                     /clone_lib="RPCI-23"
                     /sex="Female"
                     /lab_host="DH10B"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT          189 a   126 c   152 g   160 t                2 others
ORIGIN

Query Match       14.7%; Score 30.2; DB 17; Length 629;
Best Local Similarity 50.7%; Pred. No.79;
Matches 71; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY  18  GACGTATACGAGTCTTTGGTCAAATTCCAGGACACAGATGATCGGTCCAAGAACAGGAT 77
      ||| ||||| |
Db   493  GATCTTTGTGAGCAANAGAGTGTTGCCAGGACAGCCAGGACTCTGTTACACAGAGGGAA 434
      ||| ||||| |

QY  78  AATAGAACTAAGCAACGGCATACAATTTGGGTGGATTGGCAACAAAACCTTCTGTGACTAA 137
      ||| ||||| |
Db   433  ACCCTGTCTTGAAAAATGACACAGAATTATATACTTAGCCCCCATGAAGATTCTTGAGGGCTAA 374
      ||| ||||| |

QY  138  CAGGTCCATAGTTTTTTCACG 157
      ||| ||||| |
Db   373  CAAGCACATACATGTTTCAAG 354

```

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 513)
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman
,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
JOURNAL Mol. Vis. 8 (4), (2002) In press
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 09 row: c column: 01
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
source
1. 513
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="he09c01"
/clone_lib="Human Retina cDNA (Un-normalized, unamplified
); hd/he"
/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (<http://www.lifetech.com/>). First
strand synthesis was carried out using a Not I
primer-adaptor [5'-pGACTAGTTCTAGATCGGCGGCCG(T)15-3',
]. EST analysis was performed on the unamplified library
at the NIH Intramural Sequencing Center (NISC)."
BASE COUNT 171 a 85 c 92 g 165 t
ORIGIN
Query Match 14.6%; Score 30; DB 14; Length 513;
Best Local Similarity 53.4%; Pred. No. 83;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 6 AGCCATGGTATGACGATATACGAGTCTTGGTCAATTTCCAGGACACAGATGATCGGTC 65
Db 297 ACCAATGACATGGATAATTTAGAGTACTATTATTTGTCTACCACACAGATATGTCCTC 238
QY 66 CAAGAACAGGATAATAGAACTAAGCAACGCCGATACAAATTTGGTGGATGGCAACAAA 123
Db 237 CAAAATCAATGCAATAATCTAAATAAATGATAAAAAATTTATGTTTGGAGAATAAA 180
RESULT 56
BG384279/c
LOCUS BG384279 519 bp mRNA linear EST 12-MAR-2001
DEFINITION 303302 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG384279
VERSION BG384279.1 GI:13308751
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 519)
AUTHORS Fahrénkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.

and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: E column: 21
Seq primer: ATTAGGTGACACTATAG.
FEATURES
source
1. 519
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 159 a 96 c 118 g 146 t
ORIGIN
Query Match 14.6%; Score 30; DB 12; Length 519;
Best Local Similarity 52.4%; Pred. No. 84;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 78 AATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTTCTGTGACTAA 137
Db 175 ACTCAAAGAAGGAGTGCTCTACAAACGGCTTTTACTCACTACGAAGTTCTTGGGATAAA 116
QY 138 CAGGTCCATAGTTTTTTCAGCACACTTCCAAGGACGCCATACCGAACAACAAAGGTGTTA 197
Db 115 TGTGTTTATATTTTGAAGTGAACGGTCACATGATGTCGTAATCATGCCAGCCATTGATCA 56
QY 198 TTATCC 203
Db 55 CTATCC 50
RESULT 57
BH305658
LOCUS BH305658 631 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-179016.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-179016, DNA sequence.
ACCESSION BH305658
VERSION BH305658.1 GI:17218066
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 631)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment
JOURNAL Unpublished (1999)
COMMENT Other GSSs: CH230-179016.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 179 row: O column: 16
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1. .631
/organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-179O16"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"

BASE COUNT 237 a 74 c 124 g 196 t

ORIGIN

Query Match 14.6%; Score 30; DB 17; Length 631;
Best Local Similarity 61.5%; Pred. No. 92;
Matches 48; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 77 TAATAGAACTAAGCAACGGATACAAATTGGTGGATTGGCAACAAACTTCCTGTGACTA 136

Db 194 TAATATAACTATTCAATAAAATTAAATTTGCTTCATATACTTCTTAACCTTACTCTTACAA 253

QY 137 ACAGTCCATAGTTTTC 154

Db 254 ATATATCTATAATTTTAC 271

RESULT 58

BH200757

LOCUS

DEFINITION BH200757 697 bp DNA linear GSS 24-OCT-2001
Sml-45018.TR Sml Schistosoma mansoni genomic clone Sml-45018, DNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Schistosoma mansoni.

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 697)

Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed

,N.M.

Use of end sequences from Schistosoma mansoni (Puerto Rico strain)

Sml BAC library for gene discovery and map construction

Unpublished (2001)

COMMENT

Other GSSs: Sml-45018.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: nelsayed@tigr.org

lo.edu).

Seq primer: M13 Rev

Class: BAC ends.

Location/Qualifiers

1. .697

/organism="Schistosoma mansoni"

/strain="Puerto Rico"

/db_xref="taxon:6183"

FEATURES

source

/clone="Sml-45018"

/clone_lib="Sml"

/note="Vector: pBeloBAC11; Site 1: Hin dIII; Constructed
in the laboratory of Dr. Denis Le Paslier at the Fondation
Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
mansoni agarose embedded DNA was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBeloBAC11 digested with Hin dIII. The average insert size
is 100 kb. Total clone coverage: approx. 7.95 X the
haploid genome. Further information can be found in Le
Paslier et al. (2000) Construction and characterization of
a Schistosoma mansoni bacterial artificial chromosome
library. Genomics 65: 87-94."

BASE COUNT 275 a 111 c 96 g 215 t

ORIGIN

Query Match 14.6%; Score 30; DB 17; Length 697;
Best Local Similarity 61.5%; Pred. No. 97;
Matches 48; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 10 ATGGTATGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAG 69

Db 171 ATCATATAGAATTTCATCAAAATTATTGGACAATGACTGATATACATATTAATTGGTTAAAT 230

QY 70 AACAGGATAATAGAACTA 87

Db 231 AACAGTATAATGGATCAA 248

RESULT 59

BQ250036/c

LOCUS

DEFINITION

BQ250036 313 bp mRNA linear EST 03-MAY-2002
TaE25010F12R TaE25 Triticum aestivum cDNA clone TaE25010F12R, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Triticum.

1 (bases 1 to 313)

Cloutier,S.

Wheat functional genomics - Glenlea developing seeds cDNA libraries

Unpublished (2002)

Contact: Dr. Sylvie Cloutier

Cereal Research Centre, Agriculture and Agri-food Canada

195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9

Tel: (204) 983-2340

Fax: (204) 983-4604

Email: scloutier@em.agr.ca

was cloned directionally, not all sequences generated with reverse

primer were from the 5' end (same with forward primer and 3' end).

Average insert size is >870 bp

Plate: 010 row: F column: 12

Seq primer: M13 Reverse.

Location/Qualifiers

1. .313

/organism="Triticum aestivum"

/cultivar="Glenlea"

/db_xref="taxon:4565"

/clone="TaE25010F12R"

/clone_lib="TaE25"

/tissue_type="developing seeds"

/dev_stage="25 days after anthesis"

/lab_host="E. coli DH10B"

/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);

Site 1: NotI; Site 2: MluI; mRNA obtained from wheat seeds

of cultivar Glenlea 25 days post-anthesis"

BASE COUNT 118 a 42 c 73 g 80 t

ORIGIN

Qy	21	GTATACGAGTTC TTGGTCAATTCCAGGCACACAGATGATTCGCTCCAAGAACAGGATAAT	80
Db	342	GTAACCACCTTCAGGGTCATTGCCAACATCATAAAGAGTCCTCGGAAGTATACAAAAAT	283
Qy	81	AGAACTAAGCAA CGCGATACAATTGGTGATTTGGCAACAAACTTCCTGTGACTAACAG	140
Db	282	GGACCTGGAGTCTTGT CAGGAATTAGGTGGGTATGCATTTCTGTGGTGGAGCATACGG	223
Qy	141	GTCCATAGTTTTTCACGCACACTTCCAAGGACGC	173
Db	222	AGGATGGTAATCGAGCCCTCTTTCAAGCACAC	190

RESULT 61					
BM433714					
LOCUS	BM433714	423 bp	mRNA	linear	EST 31-JAN-2002
DEFINITION	10M03H09 Bos taurus Omasum #1 library Bos taurus cdNA, mRNA				
					sequence.

ACCESSION	BM433714	
VERSION	BM433714.1	GI:18455436
KEYWORDS	EST.	
SOURCE	cow.	
ORGANISM	Bos taurus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae; Bovinae; Bos.	
REFERENCE	1 (bases 1 to 423)	

Dept of Forestry
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: smoore@afns.ualberta.ca
Insert Length: 423 Std Error: 0.00
POLYA=No.

```

/cell_type="Stratified squamous epithelial"
/dev_stage="young adult"
/lab_host="XL1-BlueMRF'strain"
/note="Organ: Omasum; Vector: Uni-2ZAPXR; Site_1: EcoRI;
Site 2: Xho I"
123 a      -70 c      85 g      145 t
BASE COUNT
ORIGIN

```

QY	148	GTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAGAAGGTGTT	196
D _b	163	TTTGACTCCTGACTTCTCAGTCTACAGAGAGATTATAACAAGACATT	211
RESULT 62			

AI975607
LOCUS AI975607 539 bp mRNA linear EST 27-AUG-1999
DEFINITION EST270201 Schistosoma mansoni female, Phil LoVerde/Joe Merrick
Schistosoma mansoni cDNA clone SMFAU96 5' end, mRNA sequence.
ACCESSION AI975607
VERSION AI975607.1 GI:5788775
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni.
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 539)
AUTHORS Merrick,J.M., Osman,A., LoVerde,P.T., Chandra,I., Glodek,A., Fraser
,C.M. and Lee,N.H.
TITLE Generation of a Schistosoma sp. EST (SMEST) Catalog & Schistosoma
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Norman H. Lee
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3529
Fax: 301 838 0208
Email: nhlee@tigr.org
Seq primer: M13 Reverse.
FEATURES
source
1..539
/organism="Schistosoma mansoni"
/db_xref="taxon:6183"
/clone="SMFAU96"
/clone_lib="Schistosoma mansoni female, Phil LoVerde/Joe
Merrick"
/sex="female"
/note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI
; directionally cloned cDNAs"
BASE COUNT 207 a 81 c 107 g 144 t
ORIGIN
Query Match 14.5%; Score 29.8; DB 9; Length 539;
Best Local Similarity 51.9%; Pred. No. 99;
Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 68 AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAACTTC 127
|||||
Db 395 AGAAAGAGAAAAATTCAACTCTTAAAGCTAATTTAATTCAGATTGAAGAGAAAAATGC 454
QY 128 CTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAAG 187
| | | | |
Db 455 TTATCAACAAAGCTTGACATTTTATCTGTTACTTTAAGAACGTTGAACCTTGACTGCA 514
QY 188 CAAGGTGTT 196
| | | | |
Db 515 GAGGGATT 523
RESULT 63
AV617820
LOCUS AV617820 Bos taurus ovary fetus Bos taurus cDNA clone E1OV013G05
DEFINITION 5', mRNA sequence.
ACCESSION AV617820
VERSION AV617820.1 GI:9753490
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 581)
AUTHORS Takauega,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
TITLE Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs

JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)
MEDLINE 21570554
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
FEATURES
source
1..581
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="E1OV013G05"
/clone_lib="Bos taurus ovary fetus"
/tissue_type="ovary"
/dev_stage="fetus"
/lab_host="DH10B"
/note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"
BASE COUNT 167 a 111 c 126 g 177 t
ORIGIN
Query Match 14.5%; Score 29.8; DB 10; Length 581;
Best Local Similarity 48.5%; Pred. No. 1e+02;
Matches 82; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 28 AGTTCCTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTA 87
| | | | |
Db 353 AGGTTGTAATCATCTCCCTTTTCACATGAGTGTGTTATGAGAACTGTGGAATGTTTAA 412
QY 88 AGCAACGCGATACAAATTTGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCATA 147
| | | | |
Db 413 ACAAACCTGAAATCTATGGGAAGGAGGAGAAAGCCTTTCTAAACCTACAGTTCTGCA 472
QY 148 GTTTTTCACGACACTTCCAAAGGAGCGCCATACCGAACAACAAAGCAAGGTGT 196
| | | | |
Db 473 TTTGGACTCCTGACTTTCTCAGTCTACAGAGAGATTATACAGACATT 521
RESULT 64
BF009213/c
LOCUS BF009213 587 bp mRNA linear EST 06-DEC-2001
DEFINITION ss75e02.y1 Gm-cl062 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl062-2259 5' similar to TR:Q9ZW45 Q9ZW45 F17L21.24.; mRNA
sequence.
ACCESSION BF009213
VERSION BF009213.1 GI:10709489
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 587)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

/db_xref="taxon:6183"
/clone="SMFBF09"
/clone_lib="Schistosoma mansoni female, Phil LoVerde/Joe
Merrick"
/sex="female"
/note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI
; directionally cloned cDNAs"
BASE COUNT 236 a 98 c 136 g 167 t
ORIGIN

Query Match 14.5%; Score 29.8; DB 9; Length 637;
Best Local Similarity 51.9%; Pred. No. 1.1e+02;
Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 68 AGAACAGGATAAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTTC 127
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 395 AGAAAGAGAAAATTCAACTCTTAAAGCTAATTTAATTCAGATTGAAGAGAAAAAATGC 454
QY 128 CTGTGACTAACAGGTCCTCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAG 187
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 455 TTATCAACAAGCTTGACATTTTATCTGTACTTTTAAAGAACGTGAACCTTGAACCTGCA 514
QY 188 CAAGGTGTT 196
||||| |||||
Db 515 GAGGGATT 523

RESULT 67
BI421295
LOCUS BI421295 638 bp mRNA linear EST 16-AUG-2001
DEFINITION EST531961 tomato callus, TAMU Lycopersicon esculentum cDNA clone
cLEC66B13 5' end, mRNA sequence.
ACCESSION BI421295
VERSION BI421295.1 GI:15194685
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 638)
AUTHORS Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning,
C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.
Location/Qualifiers
1. .638
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC66B13"
/clone_lib="tomato callus, TAMU"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 191 a 111 c 159 g 177 t
ORIGIN
Query Match 14.5%; Score 29.8; DB 13; Length 638;
Best Local Similarity 60.5%; Pred. No. 1.1e+02;
Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 68 AGAACAGGATAAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTTC 127
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 395 AGAAAGAGAAAATTCAACTCTTAAAGCTAATTTAATTCAGATTGAAGAGAAAAAATGC 454
QY 128 CTGTGACTAACAGGTCCTCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAG 187
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 455 TTATCAACAAGCTTGACATTTTATCTGTACTTTTAAAGAACGTGAACCTTGAACCTGCA 514
QY 188 CAAGGTGTT 196
||||| |||||
Db 515 GAGGGATT 523

Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 113 TTGGCAACAAACTTCTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAGGACG 172
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 TTGGTACTGAACCTTCTTGTATTGGAAAGGCAATAGAGTCTCATCTACAAATACA 117
QY 173 CCATACCGAACAAGCAAGGT 193
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 118 GCATCCTGACCAACTCATGGT 138

RESULT 68
BF046370
LOCUS BF046370 664 bp mRNA linear EST 10-OCT-2000
DEFINITION BP250021A20A7 Soares normalized bovine placenta Bos taurus cDNA
clone BP250021A20A7 5', mRNA sequence.
ACCESSION BF046370
VERSION BF046370.1 GI:10763425
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 664)
AUTHORS Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson,
J.H.

TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimming:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCTTCACTAAAG
Insert Length: 664 Std Error: 0.00
Plate: BP250021A20 row: A column: 7
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 664.
Location/Qualifiers
1. .664
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP250021A20A7"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"

/note="Organ: placenta; Vector: pT7T3Pac; Site 1: EcoRI;
Site 2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."
BASE COUNT 198 a 123 c 137 g 202 t
ORIGIN

Query Match 14.5%; Score 29.8; DB 12; Length 664;
Best Local Similarity 48.5%; Pred. No. 1.1e+02;
Matches 82; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 28 AGTTCTTGGTCAATTTCCAGGACACAGATGATTTCGGTCCAAGAACAGGATAATAAGAACTA 87
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 484 AGGTGTAATCATCTCTCCCTTTTCACATGAGTGTATTATGAGAACTGTGGATGTTTAAA 543
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 88 AGCAACGCGATACAATTTGGTGGATTGGCAACAAACTTCTGTGACTAACAGGTCCATA 147
Db 544 ACAAACTTGAAATCTATGGGAAGGAAGGAGAAAGCCTTTCTAAAACCTACAGTTCTGCA 603
QY 148 GTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAGCAAGGTGTT 196
Db 604 TTTGGACTCCTGACTTTCTCAGTCTACAGAGAGATTATAACAAGACATT 652

RESULT 69
BF936455 712 bp mRNA linear EST 22-JAN-2001
LOCUS EST459510 Schistosoma mansoni female, Phil LoVerde/Joe Merrick
DEFINITION Schistosoma mansoni cDNA clone SMFBX14 5' end, mRNA sequence.
ACCESSION BF936455
VERSION BF936455.1 GI:12353775
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 712)
AUTHORS Merrick,J.M., Osman,A., LoVerde,P.T., Cho,J., Fraser,C.M. and Lee ,N.H.
TITLE Generation of a Schistosoma sp. EST (SMEST) Catalog & Schistosome Gene Index (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Norman H. Lee
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3529
Fax: 301 838 0208
Email: nhlee@tigr.org
Seq primer: M13 reverse.
Location/Qualifiers
source 1. .712
/organism="Schistosoma mansoni"
/db_xref="taxon:6183"
/clone="SMFBX14"
/clone_lib="Schistosoma mansoni female, Phil LoVerde/Joe Merrick"
/sex="female"
/note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI ; directionally cloned cDNAs"

BASE COUNT 265 a 109 c 154 g 184 t
ORIGIN
Query Match 14.5%; Score 29.8; DB 12; Length 712;
Best Local Similarity 51.9%; Pred. No. 1.1e+02;
Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 68 AGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTTC 127
Db 395 AGAAGAGAAAATTCACACTCTTAAAGCTAATTTAATTCAGATTGAAGAGAAAAAATGC 454
QY 128 CTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAAGGACGCCATACCGAACAAG 187
Db 455 TTATCAACAAGCTTGACATTTTATCTCTGTTACTTTAAAGAACGTGAACCTTGAACCTGCA 514
QY 188 CAAGGTGTT 196
Db 515 GAGGGATT 523

RESULT 70
AZ668876 944 bp DNA linear GSS 14-DEC-2000
LOCUS ENTJR88TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.
DEFINITION AZ668876
ACCESSION AZ668876
VERSION AZ668876.1 GI:11806022
KEYWORDS GSS.

SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica
REFERENCE Eukaryota; Entamoebidae; Entamoeba.
AUTHORS 1 (bases 1 to 944)
TITLE Loftus,B., Van Aken,S. and Fraser,C.
JOURNAL Determination of clone end sequences from Entamoeba histolytica
COMMENT HM1:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 142
High quality sequence stop: 299.
Location/Qualifiers
source 1. .944
/organism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Borell, Oxford University Press, 1999)."

BASE COUNT 359 a 97 c 145 g 343 t
ORIGIN
Query Match 14.5%; Score 29.8; DB 17; Length 944;
Best Local Similarity 47.2%; Pred. No. 1.3e+02;
Matches 91; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 9 CATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATCGGTCCAA 68
Db 99 CATAAATAAGAAAGTATTATTTTCTTTTAACTTATATGGATTATCTATTCAA 158
QY 69 GAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTTCC 128
Db 159 AAAGAAATCAACTCAAAATAGTTTCAAAGGAATTTCTTTGGATTATAAAAAATATTTTA 218
QY 129 TGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAAGGACGCCATACCGAACAAGC 188
Db 219 TTATATGAAAAGGTGCCTAATTTGGTGAAAAACATGTAATAATTTGGTAAAAAATATTAAC 278
QY 189 AAGGTGTTATTAT 201
Db 279 TAACTTTCTTAT 291

RESULT 71
BQ064772/c 1002 bp mRNA linear EST 02-APR-2002
LOCUS BQ064772
DEFINITION AGENCOURT_6853665 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5926529
ACCESSION 5', mRNA sequence.
BQ064772
VERSION BQ064772.1 GI:19893720
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1002)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2099 row: p column: 18
High quality sequence start: 16
High quality sequence stop: 641.
Location/Qualifiers
1. .1002
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5926529"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
279 a 227 c 220 g 275 t 1 others
BASE COUNT 279 a 227 c 220 g 275 t 1 others
ORIGIN
Query Match 14.5%; Score 29.8; DB 14; Length 1002;
Best Local Similarity 49.7%; Pred. No. 1.3e+02;
Matches 76; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 10 ATGGTATGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAG 69
Db 939 ATGCCCTCGAAGTTTTTTTTTTTTTTTTTTTAAAAAAAAGATGTTTATTAGGAA 880
QY 70 AACAGGATAATAGAACTAAGCAACGGCATACAATTTGGTGGATTGGCAACAACTTCCT 129
Db 879 AGTATCATAGTGTAAACCAACAAATTTGTACCACCTTTGATTTTCTGGGAATACAGACTC 820
QY 130 GTGACTACAGGTCCATAGTTTTTTTCCAGCACT 162
Db 819 GTGATGCAAGCTGAAGTTGTGTGTACAAAGACT 787
RESULT 72
BH633508/c
LOCUS
DEFINITION
SALK_042693 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_042693, DNA sequence.
ACCESSION
BH633508
VERSION
BH633508.1 GI:18468871
KEYWORDS
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 424)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
REFERENCE
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1002)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2099 row: p column: 18
High quality sequence start: 16
High quality sequence stop: 641.
Location/Qualifiers
1. .1002
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5926529"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
279 a 227 c 220 g 275 t 1 others
BASE COUNT 279 a 227 c 220 g 275 t 1 others
ORIGIN
Query Match 14.5%; Score 29.8; DB 14; Length 1002;
Best Local Similarity 49.7%; Pred. No. 1.3e+02;
Matches 76; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 10 ATGGTATGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAG 69
Db 939 ATGCCCTCGAAGTTTTTTTTTTTTTTTTTTTAAAAAAAAGATGTTTATTAGGAA 880
QY 70 AACAGGATAATAGAACTAAGCAACGGCATACAATTTGGTGGATTGGCAACAACTTCCT 129
Db 879 AGTATCATAGTGTAAACCAACAAATTTGTACCACCTTTGATTTTCTGGGAATACAGACTC 820
QY 130 GTGACTACAGGTCCATAGTTTTTTTCCAGCACT 162
Db 819 GTGATGCAAGCTGAAGTTGTGTGTACAAAGACT 787
RESULT 72
BH633508/c
LOCUS
DEFINITION
SALK_042693 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_042693, DNA sequence.
ACCESSION
BH633508
VERSION
BH633508.1 GI:18468871
KEYWORDS
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 424)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1002)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2099 row: p column: 18
High quality sequence start: 16
High quality sequence stop: 641.
Location/Qualifiers
1. .1002
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5926529"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
279 a 227 c 220 g 275 t 1 others
BASE COUNT 279 a 227 c 220 g 275 t 1 others
ORIGIN
Query Match 14.5%; Score 29.8; DB 14; Length 1002;
Best Local Similarity 49.7%; Pred. No. 1.3e+02;
Matches 76; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 10 ATGGTATGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAG 69
Db 939 ATGCCCTCGAAGTTTTTTTTTTTTTTTTTTTAAAAAAAAGATGTTTATTAGGAA 880
QY 70 AACAGGATAATAGAACTAAGCAACGGCATACAATTTGGTGGATTGGCAACAACTTCCT 129
Db 879 AGTATCATAGTGTAAACCAACAAATTTGTACCACCTTTGATTTTCTGGGAATACAGACTC 820
QY 130 GTGACTACAGGTCCATAGTTTTTTTCCAGCACT 162
Db 819 GTGATGCAAGCTGAAGTTGTGTGTACAAAGACT 787
RESULT 72
BH633508/c
LOCUS
DEFINITION
SALK_042693 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_042693, DNA sequence.
ACCESSION
BH633508
VERSION
BH633508.1 GI:18468871
KEYWORDS
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 424)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At2g45620.
Class: TDNA tagged.
Location/Qualifiers
1. .424
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_042693"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 97 a 139 c 71 g 117 t
ORIGIN
Query Match 14.4%; Score 29.6; DB 17; Length 424;
Best Local Similarity 51.5%; Pred. No. 1e+02;
Matches 68; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 15 ATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAG 74
Db 389 AAGGAGGTTATGATTACTGGTCCGATGACCGTTAGATTCCCAATTCGACGGAGGAAAAAG 330
QY 75 GATAATAGAACTAAGCAACGGCATACAATTTGGTGGATTGGCAACAACTTCCTGTGAC 134
Db 329 GATTATTGACGGTAGGACCAATGGCTGCGATGGCTGGATCGAGAGCGAATGACTGATGAT 270
QY 135 TAACAGGTCCAT 146
Db 269 GCTGAGGACCTT 258
RESULT 73
BH633544/c
LOCUS
DEFINITION
SALK_042739 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_042739, DNA sequence.
ACCESSION
BH633544
VERSION
BH633544.1 GI:18468907
KEYWORDS
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 454)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
REFERENCE
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At2g45620.

Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..454
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_042739"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 100 a 142 c 75 g 137 t
ORIGIN
Query Match 14.4%; Score 29.6; DB 17; Length 454;
Best Local Similarity 51.5%; Pred. No. 1.1e+02;
Matches 68; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 15 ATGGACGTATACGAGTTCTTGGTCAATTCCAGGACACAGATGATTCGGTCCAGAACAG 74
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 AAGGAGGGTTATGATTACTGGTTCGATGACCGTTAGATTGCCAATTCGACGGAGGAAAG 243
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 75 GATAATAGAACTAAGCAACGCGATACAAATTGGGTGGATTGGCAACAAACTTCCTGTGAC 134
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 242 GATTATTGACGGTAGGACCAATGGCTGCGATGGCTGGATCGAGAGCGAATGACTGATGAT 183
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 135 TAACAGGTCCAT 146
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 GCTGAGGACCTT 171
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RESULT 74
BI004390
LOCUS BI004390 474 bp mRNA linear EST 13-JUN-2001
DEFINITION MR4-HN0054-060301-003-g11 HN0054 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI004390
VERSION BI004390.1 GI:14408464
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 474)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-HN0054-060301-003-g11&t3=2001-03-06&t4=1>)
Seq primer: puc 18 forward

High quality sequence start: 32
High quality sequence stop: 228.

FEATURES
source

Location/Qualifiers
1..474
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HN0054"
/dev_stage="Adult"
/note="Organ: head normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 116 a 126 c 118 g 114 t
ORIGIN

Query Match 14.4%; Score 29.6; DB 13; Length 474;
Best Local Similarity 59.5%; Pred. No. 1.1e+02;
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 72 CAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAACTTCCTGT 131
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5 CACGATAATTGGAGGAAGGTTCCAGACTCAAAGGTGATCTATCGACGCCAATGCTCCTGT 64
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 132 GACTAACAGGTCCTAGTTTTTCA 155
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 GGCTGTGATCCAAAGTTCCTGA 88
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 75
BF731738/c

LOCUS BF731738 498 bp mRNA linear EST 01-AUG-2002
DEFINITION 3092-33 hindgut and Malpighian tubule subtracted cDNA library
Ctenocephalides felis cDNA clone 3092-33, mRNA sequence.

ACCESSION BF731738
VERSION BF731738.1 GI:22038887
KEYWORDS EST.
SOURCE cat flea.

ORGANISM Ctenocephalides felis
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Siphonaptera; Pulicidae; Pulicinae;
Ctenocephalides.
REFERENCE 1 (bases 1 to 498)
AUTHORS Gaines, P.J., Brandt, K.S., Eisele, A.M., Wagner, W.P., Bozic, C.M. and
Wisniewski, N.

TITLE Analysis of expressed sequence tags from subtracted and
unsubtracted C. felis hindgut and Malpighian tubule cDNA libraries
JOURNAL Unpublished (2001)

COMMENT

Contact: Gaines, Patrick J.
Pharmaceutical Discovery Group
Heska Corporation
1613 Prospect Parkway, Fort Collins, CO 80525 USA
Tel: 970 493-7272
Fax: 970 472-1644
Email: gainesp@heska.com
Seq primer: CGA GCT CGG ATC CAC TAG.

FEATURES
source

Location/Qualifiers
1..498
/organism="Ctenocephalides felis"
/db_xref="taxon:7515"
/clone="3092-33"
/clone_lib="hindgut and Malpighian tubule subtracted cDNA
library"
/sex="female and male (4:1 ratio)"
/tissue_type="hindgut and Malpighian tubule"
/dev_stage="unfed adult and 24 hour cat blood-fed adults
(1:1 ratio)"
/note="The library was made using the PCR-Select (cDNA
Subtraction kit (CLONTECH Laboratories, Inc.) with 2 (g
hindgut and Malpighian tubule mRNA used as to make the
'tester' cDNA and 2 (g carcass (all flea tissues minus

the hindgut and Malpighian tubules) to make the 'driver' cDNA. Suppression PCR and subtractive hybridization techniques are then used to enrich for cDNAs in the tester pool that are not also present in the driver pool.

BASE COUNT 164 a 84 c 88 g 153 t 9 others
ORIGIN

Query Match 14.4%; Score 29.6; DB 12; Length 498;
Best Local Similarity 54.6%; Pred. No. 1.1e+02;
Matches 53; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 39 AATTTCAGGACACAGATGATTTCGGTCCAAAGAACAGGATAATAGAACTAAGCAACGCGAT 98
Db 498 AATGTAGCTCAAACTGATAATGCTCACCATGAACAGAAATTATGGANCTTTNATATNGGAN 439

QY 99 ACAATTTGGGTGGATTGGCAACAACTTCCTGTGACT 135
Db 438 ACACTGATGTTTNNACGGCTTCAAATCTGGTGTGAAT 402

Search completed: February 15, 2003, 23:10:31
Job time : 1202 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
OM protein - protein search, using sw model
Run on: February 11, 2003, 08:36:01 ; Search time 29 Seconds
(without alignments)
404.989 Million cell updates/sec

Title: 09-833799-13B
Perfect score: 327
Sequence: 1 aqepvkgpvstkgpcpiil.....cpgikkcccgscgmcfvpq 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL 21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rviro:
16: sp_bacteriaph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Match %	Length	ID	Description		
1	250	76.5	134	6	O46625	O46625 bos taurus	
2	217.5	66.5	139	6	Q9XS42	Q9XS42 phacochoeru	
3	216.5	66.2	143	6	Q29127	Q29127 sus scrofa	
4	201	61.5	153	6	Q9XS44	Q9XS44 tayassu taj	
5	182	55.7	89	6	O46643	O46643 macaca mula	
6	181.5	55.5	207	6	Q9XS43	Q9XS43 phacochoeru	
7	177.5	54.3	181	6	P79389	P79389 sus scrofa	
8	171	52.3	131	11	Q9R028	Q9R028 rattus norv	
9	170	52.0	96	6	O62652	O62652 bos taurus	
10	166	50.8	180	6	Q9XS45	Q9XS45 hippopotamu	
11	160.5	49.1	130	11	Q9WUQ4	Q9WUQ4 rattus norv	
12	158	48.3	76	11	Q91VF8	Q91VF8 cavia porce	
13	135	41.3	114	6	Q9XS46	Q9XS46 sus scrofa	
14	131	40.1	1557	11	Q8VID9	Q8VID9 cavia porce	
15	121.5	37.2	224	4	Q8TCV5	Q8TCV5 homo sapien	
16	117	35.8	2150	5	O44131	O44131 caenorhabdi	

17	116.5	35.6	3198	5	Q9U8G8	Q9u8g8 manduca sex
18	113.5	34.7	126	11	Q8VE57	Q8ve57 mus musculu
19	112	34.3	111	4	Q8WWY7	Q8wwy7 homo sapien
20	112	34.3	138	4	Q9BR31	Q9br31 homo sapien
21	110.5	33.8	262	13	Q98988	Q98988 salvelinus
22	108	33.0	96	6	O46626	O46626 bos taurus
23	108	33.0	110	6	O46627	O46627 bos taurus
24	105.5	32.3	121	13	Q91450	Q91450 salvelinus
25	105.5	32.3	188	6	Q95JH3	Q95jh3 trichosurus
26	103	31.5	232	4	Q96A34	Q96a34 homo sapien
27	103	31.5	1511	5	Q9VB21	Q9vb21 drosophila
28	102.5	31.3	903	5	O44397	O44397 trichuris t
29	102	31.2	68	6	Q97751	Q97751 sus scrofa
30	101.5	31.0	139	4	Q8TC52	Q8tc52 homo sapien
31	101.5	31.0	224	4	Q9BQP3	Q9bqp3 homo sapien
32	101	30.9	151	5	Q8WRP3	Q8wrp3 penaeus van
33	101	30.9	163	5	Q8WRP5	Q8wrp5 penaeus van
34	101	30.9	163	5	Q8WRP4	Q8wrp4 penaeus van
35	101	30.9	163	5	Q8WRP1	Q8wrp1 penaeus van
36	101	30.9	188	5	Q8WRN8	Q8wrn8 litopenaeus
37	101	30.9	522	5	Q9VCC7	Q9vcc7 drosophila
38	101	30.9	525	5	Q8WS92	Q8ws92 drosophila
39	100.5	30.7	675	13	Q9PSH7	Q9psh7 gallus gall
40	100	30.6	76	4	Q8WXW1	Q8wxw1 homo sapien
41	99.5	30.4	674	13	Q90369	Q90369 coturnix co
42	98	30.0	174	11	Q9DAU7	Q9dau7 mus musculu
43	98	30.0	421	13	Q9DEY1	Q9dey1 cyprinus ca
44	98	30.0	2174	5	Q9GQR0	Q9gqr0 drosophila
45	98	30.0	3060	5	Q9VAV4	Q9vav4 drosophila
46	97.5	29.8	1428	5	O44341	O44341 haliotis ru
47	96.5	29.5	225	11	Q99M36	Q99m36 mus musculu
48	96	29.4	123	5	Q8WRN9	Q8wrn9 litopenaeus
49	95.5	29.2	293	13	Q9DEX9	Q9dex9 cyprinus ca
50	95.5	29.2	329	13	Q9DEY0	Q9dey0 cyprinus ca
51	94.5	28.9	74	11	Q91VQ6	Q91vq6 mus musculu
52	94	28.7	73	4	Q8WXW0	Q8wxw0 homo sapien
53	92.5	28.3	662	5	O62299	O62299 caenorhabdi
54	92.5	28.3	700	5	Q8WS94	Q8ws94 caenorhabdi
55	91.5	28.0	633	13	Q9IAR3	Q9iar3 brachydanio
56	91.5	28.0	652	13	Q9IAR4	Q9iar4 brachydanio
57	91	27.8	163	5	Q8WRP2	Q8wrp2 penaeus van
58	91	27.8	169	5	Q8WRP0	Q8wrp0 penaeus van
59	90.5	27.7	475	5	Q27087	Q27087 trichuris t
60	90	27.5	141	5	Q8WRN7	Q8wrn7 litopenaeus
61	89.5	27.4	178	13	Q9IAR5	Q9iar5 fugu rubrip
62	87.5	26.8	80	11	Q9JHY4	Q9jhy4 mus musculu
63	85	26.0	472	5	Q8WS93	Q8ws93 bombyx mori
64	85	26.0	1142	5	Q26615	Q26615 strongyloce
65	83.5	25.5	85	11	Q9JHY3	Q9jhy3 mus musculu
66	82	25.1	174	5	Q9TXK3	Q9txk3 caenorhabdi
67	81.5	24.9	102	4	Q8WXXV9	Q8wxv9 homo sapien
68	81.5	24.9	212	11	O70280	O70280 rattus norv
69	80.5	24.6	201	11	Q9CQZ8	Q9cqz8 mus musculu
70	80.5	24.6	207	11	Q8R110	Q8r110 mus musculu
71	80.5	24.6	211	11	Q9ESH5	Q9esh5 mus musculu
72	80	24.5	249	5	O16701	O16701 caenorhabdi
73	79.5	24.3	168	4	Q9HAU1	Q9hau1 homo sapien
74	79.5	24.3	220	4	Q9HC57	Q9hc57 homo sapien
75	77	23.5	131	4	Q9BQY6	Q9bgy6 homo sapien
76	77	23.5	762	5	Q8T3T1	Q8t3t1 lytechinus
77	76.5	23.4	80	4	Q8WXW2	Q8wxw2 homo sapien
78	76.5	23.4	134	11	Q8R0J0	Q8r0j0 mus musculu
79	75.5	23.1	137	6	Q9BDL0	Q9bdl0 oryctolagus
80	74.5	22.8	3680	5	Q9VR08	Q9vr08 drosophila
81	73.5	22.5	1370	5	Q8T1G2	Q8tlg2 dictyosteli
82	72	22.0	548	4	Q96NZ8	Q96nz8 homo sapien
83	71	21.7	273	10	O24654	O24654 arabidopsis
84	71	21.7	1653	5	Q9VIU9	Q9viu9 drosophila
85	68.5	20.9	181	5	O44667	O44667 caenorhabdi
86	68.5	20.9	356	2	Q93H37	Q93h37 streptomyce
87	67.5	20.6	333	5	O16699	O16699 caenorhabdi
88	67.5	20.6	809	5	Q9U3W7	Q9u3w7 drosophila
89	67	20.5	168	5	Q9GZ21	Q9gz21 cryptospori

RP SEQUENCE FROM N.A.
RX MEDLINE=96215132; PubMed=8636131;
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RA Tachibana S., Hirose S.;
RT "Accelerated evolution in inhibitor domains of porcine elafin family
RT members.";
RL J. Biol. Chem. 271:7012-7018(1996).
RN [2]
RP SEQUENCE OF 29-143 FROM N.A.
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RA Tachibana S., Hirose S.;
RL J. Biol. Chem. 0:0-0(0).
DR EMBL; D50322; BAA08857.1; -.
DR EMBL; D83668; BAA12038.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 143 AA; 15373 MW; 4D6CAAC205B9FC82 CRC64;

Query Match 66.2%; Score 216.5; DB 6; Length 143;
Best Local Similarity 60.3%; Pred. No. 1.2e-21;
Matches 38; Conservative 5; Mismatches 13; Indels 7; Gaps 1;

QY 2 QEPVKG-----VSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACF 54
Db :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
81 QDPVKAQPAIKRLILLTKPGSCPRILIRCLMVNPPNRLCLSDAQCPGVKKCCGFCGKDCM 140
QY 55 VPQ 57
Db :
141 DPK 143

RESULT 4
Q9XS44 ID Q9XS44 PRELIMINARY; PRT; 153 AA.
AC Q9XS44;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Trappin (Fragment).
OS Tayassu tajacu (Collared peccary) (Pecari tajacu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Tayassuidae; Pecari.
OX NCBI_TaxID=9829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98391820; PubMed=9722657;
RA Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
RT "Evolution of the trappin multigene family in the Suidae.";
RL J. Biochem. 124:491-502(1998).
DR EMBL; AB003283; BAA77827.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR000737; Squash.
DR InterPro; IPR002098; SVP_I.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00293; SQUASHINHBTR.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00313; SVP_I; UNKNOWN_2.
FT NON_TER 1
SQ SEQUENCE 153 AA; 16367 MW; C6864A44D570271F CRC64;

Query Match 61.5%; Score 201; DB 6; Length 153;
Best Local Similarity 55.6%; Pred. No. 1.6e-19;
Matches 35; Conservative 6; Mismatches 14; Indels 8; Gaps 1;

QY 2 QEPVGPVST-----KPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMAC 53

Db 89 QDPVKAELAVRRLVLP RRKPGFCPMIKIRCALFNP NRCLTDAGCPGARKCCIGSCGKAC 148
QY 54 FVP 56
Db 149 INP 151

RESULT 5
O46643 ID O46643 PRELIMINARY; PRT; 89 AA.
AC O46643;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Strappin-2 protein precursor (Fragment).
GN STRAPPIN-2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Zeeuwen P.L.J.M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE=97400522; PubMed=9252357;
RA Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.;
RT "Identification and Sequence Analysis of Two New Members of the
RT SKALP/elafin and SPAI-2 Gene Family; Biochemical Properties of the
RT Transglutaminase Substrate Motif and Suggestions for a New
RT Nomenclature.";
RL J. Biol. Chem. 272:20471-20478(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE=96215132; PubMed=8636131;
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RA Tachibana S., Hirose S.;
RT "Accelerated evolution in inhibitor domains of porcine elafin family
RT members.";
RL J. Biol. Chem. 271:7012-7018(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE=93280175; PubMed=7685029;
RA Molhuizen H.O., Alkemade H.A., Zeeuwen P.L., de Jong G.J.,
RA Wieringa B., Schalkwijk J.;
RT "SKALP/Elafin: An Elastase Inhibitor from Cultured Human Keratinocytes
RT Purification, cDNA Sequence, and Evidence for Transglutaminase Cross-
RT linking.";
RL J. Biol. Chem. 268:12028-12032(1993).
DR EMBL; AJ223215; CAA11183.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002098; SVP_I.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00313; SVP_I; 2.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 14 POTENTIAL.
FT CHAIN 15 >89 POTENTIAL.
FT NON_TER 89
SQ SEQUENCE 89 AA; 9307 MW; B198B4863C510DE4 CRC64;

Query Match 55.7%; Score 182; DB 6; Length 89;
Best Local Similarity 97.1%; Pred. No. 3.5e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCCLKDTD 37
Db 56 PVKGPVSTKPGSCPIILIRCAMLNPPNRCCLKDTD 89

RESULT 6
Q9XS43 PRELIMINARY; PRT; 207 AA.
AC Q9XS43;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE SPAI (Trappin-1) (Fragment).
OS Phacochoerus aethiopicus (Warthog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Phacochoerus.
OX NCBI_TaxID=85517;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98391820; PubMed=9722657;
RA Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
RT "Evolution of the trappin multigene family in the Suidae.";
RL J. Biochem. 124:491-502(1998).
DR EMBL; AB003282; BAA77826.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR000737; Squash.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00293; SQUASHINHBTR.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
FT NON TER 1
SQ SEQUENCE 207 AA; 22352 MW; 0D7AD530105F0A45 CRC64;

Query Match 55.5%; Score 181.5; DB 6; Length 207;
Best Local Similarity 47.6%; Pred. No. 9.2e-17;
Matches 30; Conservative 10; Mismatches 16; Indels 7; Gaps 1;

QY 2 QEPVKGPS-----TKPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSGMACF 54
Db 145 QDPIKAQPAVQGLLFLSKRGRCPIILRCPLANPSNKCWRDYPGVKKCCGFCGKDCL 204

QY 55 VPQ 57
Db 205 YPK 207

RESULT 7
P79389 PRELIMINARY; PRT; 181 AA.
ID P79389
AC P79389;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE Elafin family member protein precursor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96215132; PubMed=8636131;
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RA Tachibana S., Hirose S.;
RT "Accelerated evolution in inhibitor domains of porcine elafin family
members.";
RL J. Biol. Chem. 271:7012-7018(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98391820; PubMed=9722657;
RA Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
RT "Evolution of the trappin multigene family in the Suidae.";

J. Biochem. 124:491-502(1998).
DR EMBL; D50323; BAA08858.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 121 181 POTENTIAL.
SQ SEQUENCE 181 AA; 19972 MW; 90A3F88638C0A1D5 CRC64;

Query Match 54.3%; Score 177.5; DB 6; Length 181;
Best Local Similarity 51.7%; Pred. No. 2.8e-16;
Matches 30; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

QY 1 AOEVPKGP-VSTKPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSGMACFVPQ 57
Db 124 AQPVPQGRLLHYKPGLCPIWIFLRCPLPKPNKWCWRDSCPCGVKMKCCGFCGNECSYPR 181

RESULT 8
Q9R0Z8 PRELIMINARY; PRT; 131 AA.
ID Q9R0Z8
AC Q9R0Z8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Secretory leukocyte protease inhibitor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=LEWIS;
RX MEDLINE=99380355; PubMed=10449524;
RA Song Xy., Zeng L., Jin W., Thompson J., Mizel D.E., Lei K.,
RA Billingham R.C., Poole A.R., Wahl S.M.;
RT "Secretory leukocyte protease inhibitor suppresses the inflammation
and joint damage of bacterial cell wall-induced arthritis.";
RL J. Exp. Med. 190:535-542(1999).
DR EMBL; AF178426; AAD51758.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 2.
DR PRINTS; PR00003; 4DISULPHCORE.
DR ProDom; PD001224; WAP; 1.
DR SMART; SM00217; WAP; 2.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
KW Protease.
SQ SEQUENCE 131 AA; 14146 MW; 73FFB1B758CC2C4B CRC64;

Query Match 52.3%; Score 171; DB 11; Length 131;
Best Local Similarity 52.8%; Pred. No. 1.6e-15;
Matches 28; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSGMACFVP 56
Db 78 PIRGPVKKKPGRCVKGKCLMLNPPNKCQNDGQCDGKYKCCGCMGKVCCLPP 130

RESULT 9
O62652 PRELIMINARY; PRT; 96 AA.
ID O62652
AC O62652;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Trappin-6 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```



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RESULT 11
Q9WUQ4
ID Q9WUQ4 PRELIMINARY; PRT; 130 AA.
AC Q9WUQ4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Secretory leukocyte protease inhibitor.
GN SLPI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SD;
RA Chen D.H., Xu X.P., Bagchi M.K., Bagchi I.C.;
RT "Molecular cloning and spatio-temporal expression of rat secretory
RT leukocyte protease inhibitor (SLPI) in the uterus.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF151982; AAD34035.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 2.
DR PRINTS; PR00003; 4DISULPHCORE.
DR ProDom; PD001224; WAP; 1.
DR SMART; SM00217; WAP; 2.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
KW Protease.
SQ SEQUENCE 130 AA; 14017 MW; A630BA3FCE3A9D9D CRC64;

Query Match 49.1%; Score 160.5; DB 11; Length 130;
Best Local Similarity 52.8%; Pred. No. 4.2e-14;
Matches 28; Conservative 4; Mismatches 20; Indels 1; Gaps

QY 4 PVKGPVSTKPGSPILLIRCAMLNPPNRLKDTDCPGIKKCCGSGCMACFVP 56
|::||| ||| :|:|||||:| | | ||||| | |
DB 78 PIRGPVK-KPGRCLKFQKCLMLNPPNKCQNDGQCDGKYKCCGCGKVCLPP 129

RESULT 12
Q91VF8
ID Q91VF8 PRELIMINARY; PRT; 76 AA.
AC Q91VF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Caltrin-like protein II precursor.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Furutani Y., Hirose S.;
RT "Evolution of caltrin-like protein.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90216715; PubMed=2324101;
RA Colonel C.E., San Agustin J., Lardy H.A.;
RT "Purification and structure of caltrin-like proteins from seminal
RT vesicle of the guinea pig.";
RL J. Biol. Chem. 265:6854-6859(1990).
DR EMBL; AB042257; BAB70710.1; -.
DR InterPro; IPR000737; Squash.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00286; PT; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 76 POTENTIAL.

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RP SEQUENCE FROM N.A.
RC TISSUE=SEMINAL VESICLE;
RX MEDLINE=99289296; PubMed=10359639;
RA Schalkwijk J., Wiedow O., Hirose S.;
RT "The trappin gene family: proteins defined by an N-terminal
transglutaminase substrate domain and a C-terminal four-disulphide
core.";
RL Biochem. J. 340:569-577(1999).
DR EMBL; AB058645; BAB79626.1; -.
DR InterPro; IPR002098; SVP 1.
DR InterPro; IPR002221; WAP_.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN_1.
DR PROSITE; PS00313; SVP_I; UNKNOWN_1.
SQ SEQUENCE 1557 AA; 163269 MW; F9047D9B3359C719 CRC64;

Query Match 40.1%; Score 131; DB 11; Length 1557;
Best Local Similarity 47.9%; Pred.No. 4.6e-09;
Matches 23; Conservative 8; Mismatches 15; Indels 2; Gaps 0

QY 11 TKPGSCPILIRCAMLNPPNRCLKTDPCGIKKCCGSC-GMACFVPQ 57
:||||| | : : : | : ||| ||| | | | | : | :
Db 1511 SKPGSCPITGQCTQTS-DSKCGSDVECPGTKKCCVGMCGMECLPIE 1557

RESULT 15
Q8TCV5
ID Q8TCV5 PRELIMINARY; PRT; 224 AA.
AC Q8TCV5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DJ211D12.5 (Novel protein containing 2 WAP-type domains.).
GN DJ211D12.5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Burton J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z93016; CAD27771.1; -.
SQ SEQUENCE 224 AA; 24238 MW; 305CC59024058F15 CRC64;

Query Match 37.2%; Score 121.5; DB 4; Length 224;
Best Local Similarity 51.0%; Pred.No. 1.4e-08;
Matches 25; Conservative 5; Mismatches 16; Indels 3; Gaps 0

QY 9 VSTKPGSCPILIRCAMLNPPNR-CLKDTCPGIKKCCGSCGMACFVP 56
||| |||| :|| :|| :|| :|| :|| :|| :|| :||
Db 74 VSVKLGSCPEDQLRC--LSPMNLCHXDSDCSGKKRCHSACGRDCRP 120

RESULT 16
O44131
ID O44131 PRELIMINARY; PRT; 2150 AA.
AC O44131;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C08G9.2 protein.
GN C08G9.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

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OC	Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX	NCBI_TaxID=7130;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99457716; PubMed=10528409;
RA	Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
RT	"Expression of lacunin, a large multidomain extracellular matrix
RT	protein, accompanies morphogenesis of epithelial monolayers in Manduca
RT	sexta.";
RL	Insect Biochem. Mol. Biol. 29:883-897(1999).
DR	EMBL; AF078161; AAF04457.1; -.

DR InterPro; IPR004094; Antistastasin.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR002223; Kunitz_BPTI
DR InterPro; IPR000884; TSPl.
DR InterPro; IPR002221; WAP.
DR Pfam; PF02822; Antistastasin; 4.

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DR      pfam; PF00047; ig; 2; BPTI; 10.
DR      pfam; PF0014; Kunitz_BPTI; 10.
DR      pfam; PF00095; wap; 1.
DR      PRINTS; PR00759; BASICPTASE.
DR      ProDom; PD000222; Kunitz_BPTI; 10.
DR      SMART; SM00408; IGC2; 2.

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DR SMART; SM00131; KU; 10.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1
DR PROSITE; PS00280; BPTI KUNITZ_1; 8.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS50092; TSP1; 1.
KW Immunoglobulin domain; Serine protease inhibitor; Signal
FT SIGNAL 1 21 POTENTIAL.
SQ SEQUENCE 3198 AA; 349364 MW; AB4ACD459C0D9134 CRC64;

Query Match 35.6%; Score 116.5; DB 5; Length 3198;
Best Local Similarity 44.9%; Pred. No. 8.5e-07;
Matches 22; Conservative 4; Mismatches 22; Indels 1;

Qy	8	PVSTKPGSCPIILIRCA	MLNPPNRLK	DTDCPGIKKCC	EGSCGMACFVP	56
	:	:	:	:	:	:
Db	2888	PVN-KTGYCPVEQASTTE	YFCPNECVDDADCR	GVGKCCARGCGRAC	AVP	2935

RESULT 18	
Q8VE57	
ID Q8VE57	PRELIMINARY; PRT; 126 AA.
AC Q8VE57;	
DT 01-MAR-2002	(TrEMBLrel. 20, Created)
2002	(TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Similar to secretory leukocyte protease inhibitor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RI submitted (Aug. 2001) to the EMBL/GenBank/DBST databases

DR EMBL; BC019734; AAH19734.1; -
 DR Submitted (DEC-2001) to the ERL
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 2.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR PRODom; PD001224; WAP.¹

DR PRODOM; PD001224; WAP; 1.
DR SMART; SM00217; WAP; 2.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 126 AA; 13839 MW; 8D10353557B2F75

Query Match	34.7 %	Score 113.5;	DB 11;	Length 126;
Best Local Similarity	44.9 %	Pred. No. 9.7e-08;		

Matches 22; Conservative 7; Mismatches 17; Indels 3; Gaps 2;

QY 9 VSTKPGSCPIILIRCAMLNP-PNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 75 VFKGKCPVDQLRC--LSPTKHMCKDSDCSGKKRCCASACGRDCRDP 121

RESULT 19

Q8WWY7 PRELIMINARY; PRT; 111 AA.

AC Q8WWY7; 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative protease inhibitor WAP2 precursor.
GN WAP2.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21638013; PubMed=11779191;

RA Lundwall A.; Clauss A.;

RT "Identification of a novel protease inhibitor gene that is highly expressed in the prostate.";

RL Biochem. Biophys. Res. Commun. 290:452-456(2002).

DR EMBL; AY037803; AAK68848.1; -.

DR InterPro; IPR002221; WAP.

DR Pfam; PF00095; wap; 1.

DR PRINTS; PR00003; 4DISULPHCORE.

DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_1.

KW Signal; Protease.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 111 PUTATIVE PROTEASE INHIBITOR WAP2.

SQ SEQUENCE 111 AA; 12050 MW; 2DFB39043F1A0997 CRC64;

Query Match 34.3%; Score 112; DB 4; Length 111;

Best Local Similarity 42.9%; Pred. No. 1.4e-07;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQEPVKGVPSTKPGSCPIILIRCAMLNP-PNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCKSDPP-QCHTDQDCLGERKCCYLHCGFKCVP 73

RESULT 20

Q9BR31 PRELIMINARY; PRT; 138 AA.

AC Q9BR31; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE DJ211D12.4 (Similar to Elafin-like protein from mouse and WAP-type

protease inhibitors.) (Fragment).

GN C20ORF122.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Burton J.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z93016; CAC36291.2; -.

FT NON TER 1 1

SQ SEQUENCE 138 AA; 14770 MW; D4EAAEA08B79686B CRC64;

Query Match

Best Local Similarity 34.3%; Score 112; DB 4; Length 138;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQEPVKGVPSTKPGSCPIILIRCAMLNP-PNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 47 AVEGVKEGIE-KAGVCPADNVRCKSDPP-QCHTDQDCLGERKCCYLHCGFKCVP 100

RESULT 21

Q98988 PRELIMINARY; PRT; 262 AA.

AC Q98988; 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Ovulatory protein-2 precursor.

OS Salvelinus fontinalis (Brook trout) (Brook char).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.

OX NCBI_TaxID=8038;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=OVARY;

RA Garczynski M.A.; Goetz F.W.;

RT "Molecular characterization of a ribonucleic acid transcript that is highly up-regulated at the time of ovulation in the brook trout

(Salvelinus fontinalis) ovary.";

RL Biol. Reprod. 0:0-0(1997).

DR EMBL; U67854; AAB63598.1; -.

DR HSSP; P19957; 2REL.

DR InterPro; IPR002221; WAP.

DR Pfam; PF00095; wap; 5.

DR PRINTS; PR00003; 4DISULPHCORE.

DR ProDom; PD001224; WAP; 1.

DR SMART; SM00217; WAP; 3.

DR PROSITE; PS00317; 4_DISULFIDE_CORE; 5.

KW Signal.

FT SIGNAL 1 30 POTENTIAL.

FT CHAIN 31 262 OVULATORY PROTEIN-2.

SQ SEQUENCE 262 AA; 28200 MW; D2EC50FFAFECF807 CRC64;

Query Match

Best Local Similarity 33.8%; Score 110.5; DB 13; Length 262;

Matches 25; Conservative 3; Mismatches 13; Indels 17; Gaps 4;

QY 7 GPVST-KPGSCPIILIR-----CAMLPPNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 28 GGISTAKPGVCP---RRRWGIGICAEEL-----CSKSDCDPNDKCKCHNGCGHVCIAIP 76

RESULT 22

O46626 PRELIMINARY; PRT; 96 AA.

AC O46626; 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE BTRAPPIN-4 protein precursor (Fragment).

GN BTRAPPIN-4.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=TONGUE;

RA Zeeuwen P.L.J.M.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=TONGUE;

RX MEDLINE=97400522; PubMed=9252357;

RA Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.;

RT "Identification and Sequence Analysis of Two New Members of the

RT SKALP/elafin and SPAI-2 Gene Family; Biochemical Properties of the
RT Transglutaminase Substrate Motif and Suggestions for a New
RT Nomenclature.";
RL J. Biol. Chem. 272:20471-20478(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=TONGUE;
RX MEDLINE=93280175; PubMed=7685029;
RA Molhuizen H.O., Alkemade H.A., Zeeuwen P.L., de Jongh G.J.,
RA Wieringa B., Schalkwijk J.;
RT "SKALP/Elafin: An Elastase Inhibitor from Cultured Human Keratinocytes
RT Purification, cDNA Sequence, and Evidence for Transglutaminase Cross-
RT linking.";
RL J. Biol. Chem. 268:12028-12032(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=TONGUE;
RX MEDLINE=96215132; PubMed=8636131;
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RA Tachibana S., Hirose S.;
RT "Accelerated evolution in inhibitor domains of porcine elafin family
RT members.";
RL J. Biol. Chem. 271:7012-7018(1996).
DR EMBL; AJ223217; CAA11185.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
KW Signal.
FT NON TER 1 1
FT SIGNAL <1 15 POTENTIAL.
FT CHAIN 16 >96 POTENTIAL.
FT NON TER 96 96
SQ SEQUENCE 96 AA; 10145 MW; 33A8C146E0E6AEC1 CRC64;

Query Match 33.0%; Score 108; DB 6; Length 96;
Best Local Similarity 45.5%; Pred.No. 4.1e-07;
Matches 20; Conservative 7; Mismatches 7; Indels 10; Gaps 1;

QY 2 QEPVKGP-----VSTKPGSCPIILIRCAMLNPPNRCCLKD 35
|:||||| : ||||| :| :|:|||||:
Db 51 QDPVKGQDVVVQAQDRARLPFKLGSCPRVLFKCLVMNPPNRCCLR 94

RESULT 23
O46627
ID O46627 PRELIMINARY; PRT; 110 AA.
AC O46627;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Btrappin-5 protein precursor (Fragment).
GN BTRAPPIN-5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONGUE;
RX MEDLINE=97400522; PubMed=9252357;
RA Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.;
RT "Identification and Sequence Analysis of Two New Members of the
RT SKALP/elafin and SPAI-2 Gene Family; Biochemical Properties of the
RT Transglutaminase Substrate Motif and Suggestions for a New
RT Nomenclature.";
RL J. Biol. Chem. 272:20471-20478(1997).
RN [3]

RP SEQUENCE FROM N.A.
RC TISSUE=TONGUE;
RX MEDLINE=93280175; PubMed=7685029;
RA Molhuizen H.O., Alkemade H.A., Zeeuwen P.L., de Jongh G.J.,
RA Wieringa B., Schalkwijk J.;
RT "SKALP/Elafin: An Elastase Inhibitor from Cultured Human Keratinocytes
RT Purification, cDNA Sequence, and Evidence for Transglutaminase Cross-
RT linking.";
RL J. Biol. Chem. 268:12028-12032(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=TONGUE;
RX MEDLINE=96215132; PubMed=8636131;
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RA Tachibana S., Hirose S.;
RT "Accelerated evolution in inhibitor domains of porcine elafin family
RT members.";
RL J. Biol. Chem. 271:7012-7018(1996).
DR EMBL; AJ223218; CAA11186.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
KW Signal.
FT NON TER 1 1
FT SIGNAL <1 28 POTENTIAL.
FT CHAIN 29 >110 POTENTIAL.
FT NON TER 110 110
SQ SEQUENCE 110 AA; 11575 MW; 5F9E4D24A21318F2 CRC64;

Query Match 33.0%; Score 108; DB 6; Length 110;
Best Local Similarity 42.6%; Pred.No. 4.7e-07;
Matches 20; Conservative 7; Mismatches 10; Indels 10; Gaps 1;

QY 2 QEPVKGP-----VSTKPGSCPIILIRCAMLNPPNRCCLKDTC 38
|:||||| : ||||| :| :|:|||||:
Db 64 QDPVKGQDVVVQAQDRARLPFKLGSCPRVLFKCLVMNPPNRCCLR 110

RESULT 24
Q91450
ID Q91450 PRELIMINARY; PRT; 121 AA.
AC Q91450;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Antileukoprotease precursor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Hsu S.-Y., Goetz F.W.;
RT "Ovulation specific transcription of antileukoprotease-like mRNAs in
RT the fish ovary.";
RL (In) Fujimoto S. (eds.);
RL FRONTIERS IN ENDOCRINOLOGY - NEW ACHIEVEMENTS IN RESEARCH OF OVARIAN
RL FUNCTION, pp.183-190, Ares-Serono Symposia, Rome, Italy (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Hsu S.-Y., Goetz F.W.;
RT "Ovulation specific transcription of an antileukoprotease-like mRNA
RT in the fish ovary.";
RL (In) Unknown A. (eds.);
RL PROCEEDINGS OF THE FIFTH INTERNATIONAL SYMPOSIUM ON THE REPRODUCTIVE
RL PHYSIOLOGY OF FISH, pp.287-289, Unknown Publisher (1995).
DR EMBL; U03890; AAA03534.1; -.
DR HSSP; Q9N0L8; 1TWP.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 2.


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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026014; AAH26014.1; -.
SQ SEQUENCE 139 AA; 15081 MW; D8BEADC6D7B89FB2 CRC64;

Query Match 31.0%; Score 101.5; DB 4; Length 139;
Best Local Similarity 41.5%; Pred. No. 4.5e-06;
Matches 17; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

Qy 16 CPIILIRCAMLNPPNRCCLKDTCPCGIIKKCCGSCGMACFVP 56
|| : : : || : : : || : : : || : : : || : : : ||
Db 29 CPRVIRKQSL---KRCITDKTCPGVKKCCCTLGCNKSCVVP 66

RESULT 31
Q8WRP3
ID Q9BQP3 PRELIMINARY; PRT; 224 AA.
AC Q9BQP3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE DJ447F3.3.1 (Novel protein with WAP-type (Whey acidic protein)
DE 'four-disulfide core' domains (Isoform 1)) (Hypothetical 23.9 kDa
DE protein) (Fragment).
DE DJ447F3.3.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Stavrides G.S., Huckle E.J., Deloukas P.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050348; CAC36106.1; -.
DR EMBL; AL591713; CAC39444.1; -.
DR HSSP; Q9N0L8; 1TWP.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 4.
DR PRINTS; PR00003; 4DISULPHCORE.
DR ProDom; PD001224; WAP; 2.
DR SMART; SM00217; WAP; 4.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 4.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 224 AA; 23877 MW; 8B0AFE81DF83E8BD CRC64;

Query Match 31.0%; Score 101.5; DB 4; Length 224;
Best Local Similarity 41.5%; Pred. No. 7.1e-06;
Matches 17; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

Qy 16 CPIILIRCAMLNPPNRCCLKDTCPCGIIKKCCGSCGMACFVP 56
|| : : : || : : : || : : : || : : : || : : : ||
Db 69 CPRVIRKQSL---KRCITDKTCPGVKKCCCTLGCNKSCVVP 106

RESULT 32
Q8WRP3
ID Q8WRP3 PRELIMINARY; PRT; 151 AA.
AC Q8WRP3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
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OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYMPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid
RT shrimp.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430073; AAL36892.1; -.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 151 AA; 15265 MW; ABAEBB8BE9E21A7E CRC64;

Query Match 30.9%; Score 101; DB 5; Length 151;
Best Local Similarity 42.0%; Pred. No. 5.7e-06;
Matches 21; Conservative 4; Mismatches 23; Indels 2; Gaps 2;

Qy 1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCCLKDTCPCGIKKCCGSC 49
|| : : : || : : : || : : : || : : : || : : : ||
Db 85 AHEP-ETPVGTKPLDCPQVRPTCPRFHGPPTTCSNDYKAGLDKCCFDRC 133

RESULT 33
Q8WRP5
ID Q8WRP5 PRELIMINARY; PRT; 163 AA.
AC Q8WRP5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid
RT shrimp.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430071; AAL36890.1; -.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 163 AA; 16118 MW; 21D45A511504C35 CRC64;

Query Match 30.9%; Score 101; DB 5; Length 163;
Best Local Similarity 42.0%; Pred. No. 6.1e-06;
Matches 21; Conservative 4; Mismatches 23; Indels 2; Gaps 2;

Qy 1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCCLKDTCPCGIKKCCGSC 49
|| : : : || : : : || : : : || : : : || : : : ||
Db 97 AHEP-ETPVGTKPLDCPQVRPTCPRFHGPPTTCSNDYKAGLDKCCFDRC 145

RESULT 34
Q8WRP4
ID Q8WRP4 PRELIMINARY; PRT; 163 AA.
AC Q8WRP4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
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OX NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYMPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid shrimp."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430072; AAL36891.1; -.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 163 AA; 16207 MW; 67FFF8D210BE3CFC CRC64;

Query Match 30.9%; Score 101; DB 5; Length 163;
Best Local Similarity 42.0%; Pred. No. 6.1e-06;
Matches 21; Conservative 4; Mismatches 23; Indels 2; Gaps 2;

QY 1 AQEPVKGPVSTKPGSCPILIRCAMLN-PPNRCLKDTCPCGIKKCEGSC 49
Db 97 AHEP-ETPVGKPLDCPQVRPTCPFRFHGPTTCSNDYKACGLDKCCFDRC 145

RESULT 35
Q8WRP1 ID Q8WRP1 PRELIMINARY; PRT; 163 AA.
AC Q8WRP1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYMPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid shrimp."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430075; AAL36894.1; -.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 163 AA; 16148 MW; 3C145A5108C445F5 CRC64;

Query Match 30.9%; Score 101; DB 5; Length 163;
Best Local Similarity 42.0%; Pred. No. 6.1e-06;
Matches 21; Conservative 4; Mismatches 23; Indels 2; Gaps 2;

QY 1 AQEPVKGPVSTKPGSCPILIRCAMLN-PPNRCLKDTCPCGIKKCEGSC 49
Db 97 AHEP-ETPVGKPLDCPQVRPTCPFRFHGPTTCSNDYKACGLDKCCFDRC 145

RESULT 36
Q8WRN8 ID Q8WRN8 PRELIMINARY; PRT; 188 AA.
AC Q8WRN8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Litopenaeus setiferus (white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=64468;
```

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYMPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid shrimp."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430078; AAL36897.1; -.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 188 AA; 17939 MW; F7BE67BF49D2E20C CRC64;

Query Match 30.9%; Score 101; DB 5; Length 188;
Best Local Similarity 42.0%; Pred. No. 7e-06;
Matches 21; Conservative 4; Mismatches 23; Indels 2; Gaps 2;

QY 1 AQEPVKGPVSTKPGSCPILIRCAMLN-PPNRCLKDTCPCGIKKCEGSC 49
Db 122 AHEP-ETPVGKPLDCPQVRPTCPFRFHGPTTCSNDYKACGLDKCCFDRC 170

RESULT 37
Q9VCC7 ID Q9VCC7 PRELIMINARY; PRT; 522 AA.
AC Q9VCC7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CG6173 protein.
GN CG6173.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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RESULT 41

Q90369 ID Q90369 PRELIMINARY; PRT; 674 AA.
AC Q90369;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE KAL protein.
GN KAL.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94010957; PubMed=8406507;
RA Legouis R., Cohen-Salmon M., del Castillo I., Levilliers J., Capy L.,
RA Mornow J.P., Petit C.;
RT "Characterization of the chicken and quail homologues of the human
RT gene responsible for the X-linked Kallmann syndrome.";
RL Genomics 17:516-518(1993).
DR EMBL; L13976; AAA88500.1; -.
DR HSP; P19957; 2REL.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SQ SEQUENCE 674 AA; 76439 MW; 52ACDB45C75C0392 CRC64;

Query Match 30.4%; Score 99.5; DB 13; Length 674;

Best Local Similarity 31.8%; Pred. No. 3.8e-05;

Matches 21; Conservative 7; Mismatches 17; Indels 21; Gaps 2;

QY 3 EPVKGVPSTKPGSCPIILIRCAMLPPNR-----CLKOTDCPGIKKCEGSCGM 51
Db 115 EFLKYILSVKQGDGP-----APEKASGFAAACFESCEADSECSGVKKCCSNGCGH 164

QY 52 ACFVPQ 57

Db 165 TCQVPK 170

RESULT 42

Q9DAU7 ID Q9DAU7 PRELIMINARY; PRT; 174 AA.
AC Q9DAU7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 1600023A02RIK protein (WAP domain protein HE4).
GN 1600023A02RIK OR HE4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PLACENTA;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Bingle C.D.;
RT "Cloning of mouse HE4.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AK005519; BAB24094.1; -.
DR EMBL; AF334269; AAL73189.1; -.
DR HSSP; O46655; 1CJH.
DR MGD; MGI:1914951; 1600023A02RIK.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 2.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 2.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SQ SEQUENCE 174 AA; 18031 MW; 82484E28ED6F1E20 CRC64;

Query Match 30.0%; Score 98; DB 11; Length 174;

Best Local Similarity 33.8%; Pred. No. 1.7e-05;

Matches 25; Conservative 7; Mismatches 18; Indels 24; Gaps 4;

QY 3 EPVKGVPSTKP-----GSCPII-----LIRCAMLPPNRCLKDTDCPGIKKC 44
Db 105 KPPGGQVSTKPPAVTREGLVREKQGTCPSPVDIPKLGLC-----EDQCQVDSQSGNMKC 159
QY 45 CEGSCG-MACFVPQ 57
Db 160 CRNGCGKMACTTPK 173

RESULT 43

Q9DEY1 ID Q9DEY1 PRELIMINARY; PRT; 421 AA.
AC Q9DEY1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ovarian fibroin-like substance-1.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang Y.-S., Huang F.-L.;
RT "Transglutaminase activity is required to recruit fibroin-like
RT substance to fertilization envelope for adhesion of carp eggs.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF309414; AAG25716.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SQ SEQUENCE 421 AA; 38510 MW; 99698CF275C6FED7 CRC64;

Query Match

Best Local Similarity 30.0%; Score 98; DB 13; Length 421;

Matches 35.5%; Pred. No. 3.9e-05;

Query Match 29.5%; Score 96.5; DB 11; Length 225;
Best Local Similarity 37.7%; Pred. No. 3.4e-05;
Matches 20; Conservative 1; Mismatches 15; Indels 17; Gaps 2;

Qy 12 KPGSCPIILIRCAMLNPP-----NRCLKDTCPCGKIKKCEGSCGMACFVP 56
Db 180 KPGACP-----KPPRPSFGTCDECTGDCSGNMXKCCSGNGCGHACKPP 223

RESULT 48
Q8WRN9 PRELIMINARY; PRT; 123 AA.
AC Q8WRN9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Litopenaeus setiferus (white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=64468;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid shrimp."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430077; AAL36896.1; -.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SQ SEQUENCE 123 AA; 13103 MW; 71249D81F6AD5B9 CRC64;

Query Match 29.4%; Score 96; DB 5; Length 123;
Best Local Similarity 41.7%; Pred. No. 2.2e-05;
Matches 20; Conservative 4; Mismatches 22; Indels 2; Gaps 2;

Qy 3 EPVKGVPSTKPGSCPIILIRCAMLN-PNRLKDTDCPGIKKCEGSC 49
Db 61 EP-EAPVGTKLDCPQVRPTCPFRHGPVTCSSDYKCGGVDKCCFDRC 107

RESULT 49
Q9DEX9 PRELIMINARY; PRT; 293 AA.
AC Q9DEX9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ovarian fibroin-like substance-3.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang Y.-S., Huang F.-L.;
RT "Transglutaminase activity is required to recruit fibroin-like substance to fertilization envelope for adhesion of carp eggs."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309416; AAG25718.1; -.
DR HSSP; Q9N0L8; 1TWP.
DR InterPro; IPR002395; Kininogen.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00334; KININOGEN.
DR PRINTS; PR01583; KV34CHANNEL.

DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 293 AA; 27578 MW; ED8E220C4B6C2263 CRC64;

Query Match 29.2%; Score 95.5; DB 13; Length 293;
Best Local Similarity 36.7%; Pred. No. 6e-05;
Matches 18; Conservative 7; Mismatches 17; Indels 7; Gaps 2;

Qy 10 STKPGSCPI--ILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVP 56
Db 31 TVKPGQCPLEMIPPCAA-----SCFRDGGCPATQKCCPTTSGFACSEP 74

RESULT 50
Q9DEY0 PRELIMINARY; PRT; 329 AA.
AC Q9DEY0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ovarian fibroin-like substance-2 (Fragment).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang Y.-S., Huang F.-L.;
RT "Transglutaminase activity is required to recruit fibroin-like substance to fertilization envelope for adhesion of carp eggs."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309415; AAG25717.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
FT NON TER 1
SQ SEQUENCE 329 AA; 31521 MW; 36467E1929CEC8A4 CRC64;

Query Match 29.2%; Score 95.5; DB 13; Length 329;
Best Local Similarity 43.4%; Pred. No. 6.7e-05;
Matches 23; Conservative 3; Mismatches 16; Indels 11; Gaps 3;

Qy 8 PVSTKPGSCP----IILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVP 56
Db 40 PVSMPKPGQCPDPKKIPL--CA-----KSCVDDGQCPTQKCCPTTRGHACSEP 85

RESULT 51
Q91VQ6 PRELIMINARY; PRT; 74 AA.
AC Q91VQ6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to extracellular proteinase inhibitor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010986; AAH10986.1; -.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SQ SEQUENCE 74 AA; 7759 MW; 42BDCAD68303B3D3 CRC64;

Query Match 28.9%; Score 94.5; DB 11; Length 74;
Best Local Similarity 37.7%; Pred. No. 2.2e-05;
Matches 20; Conservative 1; Mismatches 15; Indels 17; Gaps 2;

QY 12 KPGSCPIILIRCAMLNPPNR-----CLKDTCPCGIIKKCCGSCGMACFVP 56
Db 29 KPGACP-----KPPPRSFGTDEQCTGDCSGNMKCCSNGCGHACKPP 72

RESULT 52
Q8WXW0 Q8WXW0 PRELIMINARY; PRT; 73 AA.
AC Q8WXW0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE WAP domain containing protein HE4-V3.
GN WFDC2.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RA Bingle C.D., Bingle L.;
RT "Novel splice variants of the human HE4 gene are expressed in
RT pulmonary epithelial cells."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF330261; AAL37487.1; --
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SQ SEQUENCE 73 AA; 8120 MW; BDCFECA4FE8D59 CRC64;

Query Match 28.7%; Score 94; DB 4; Length 73;
Best Local Similarity 34.8%; Pred. No. 2.5e-05;
Matches 24; Conservative 6; Mismatches 25; Indels 14; Gaps 3;

QY 2 QEPVKGVPSTKP-----GSCPIILIRCAMLN-PPNRCLKDTCPCGIIKKCCGS 48
Db 3 QVQVNLVPSPLPTYPVSPFPYDPKEGSCPQVNFPPQLGLCRDQCQVDSQCPGMKCCRN 62

QY 49 CG-MACFVP 56
Db 63 CGKVSCVTP 71

RESULT 53
O62299 O62299 PRELIMINARY; PRT; 662 AA.
AC O62299;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE K03D10.1 protein.
GN K03D10.1.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";

RL Science 282:2012-2018(1998).
DR EMBL; Z81561; CAB04551.1; --
DR HSSP; Q9N0L8; ITWP.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 662 AA; 74166 MW; 9199A76E8C9117B7 CRC64;

Query Match 28.3%; Score 92.5; DB 5; Length 662;
Best Local Similarity 34.0%; Pred. No. 0.00034;
Matches 17; Conservative 6; Mismatches 18; Indels 9; Gaps 2;

QY 12 KPGSCPIIL-----IRCAMLNPPNRCLKDTCPCGIIKKCCGSCGMACFVPQ 57
Db 65 KPGACPSVSNQSNYECSAL-----CQMDGECPEPTQKCCSSGCSRQCLKPR 109

RESULT 54
Q8WS94 Q8WS94 PRELIMINARY; PRT; 700 AA.
AC Q8WS94;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KAL-1.
GN KAL-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

RP SEQUENCE FROM N.A.
RA Rugarli E.I., Di Schiavi E., Ghezzi C., Ballabio A., Bazzicalupo P.;
RT "Invertebrate homologs of the Kallmann syndrome gene."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342986; AAL73338.1; --
DR InterPro; IPR003961; FN III.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SQ SEQUENCE 700 AA; 78584 MW; 2975913064E981E8 CRC64;

Query Match 28.3%; Score 92.5; DB 5; Length 700;
Best Local Similarity 34.0%; Pred. No. 0.00036;
Matches 17; Conservative 6; Mismatches 18; Indels 9; Gaps 2;

QY 12 KPGSCPIIL-----IRCAMLNPPNRCLKDTCPCGIIKKCCGSCGMACFVPQ 57
Db 103 KPGACPSVSNQSNYECSAL-----CQMDGECPEPTQKCCSSGCSRQCLKPR 147

RESULT 55
Q9IAR3 Q9IAR3 PRELIMINARY; PRT; 633 AA.
AC Q9IAR3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Kall.2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;

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[1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=20054095; PubMed=10585565;
RA  Ardouin O., Legouis R., Fasano L., David-Watine B., Korn H.,
RA  Hardelin J.P., Petit C.;
RT  "Characterization of the two zebrafish orthologues of the KAL-1 gene
RT  underlying X chromosome-linked Kallmann syndrome.";
RL  Mech. Dev. 90:89-94(2000).
DR  EMBL; AF163311; AAF25780.1; -.
DR  InterPro; IPR003961; FN.III.
DR  InterPro; IPR002221; WAP.
DR  Pfam; PF00041; fn3; 3.
DR  Pfam; PF00095; wap; 1.
DR  PRINTS; PR00003; 4DISULPHCORE.
DR  SMART; SM00060; FN3; 4.
DR  SMART; SM00217; WAP; 1.
DR  PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ  SEQUENCE 633 AA; 70672 MW; DAC21803F8899E03 CRC64;

Query Match 28.0%; Score 91.5; DB 13; Length 633;
Best Local Similarity 32.1%; Pred. No. 0.00044;
Matches 18; Conservative 3; Mismatches 14; Indels 21; Gaps 2;

QY 12 KPGSCPIILIRCAMLNPPNR-----CLKDTDCPGIKKCCGSCGMACFVP 56
Db 113 KQDCP-----PAQRASGFAAACVESCAQDRECSGVKKCCSNGCGHTCQSP 158

RESULT 56
Q9IAR4 PRELIMINARY; PRT; 652 AA.
ID Q9IAR4
AC Q9IAR4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Kall1.1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20054095; PubMed=10585565;
RA Ardouin O., Legouis R., Fasano L., David-Watine B., Korn H.,
RA Hardelin J.P., Petit C.;
RT "Characterization of the two zebrafish orthologues of the KAL-1 gene
RT underlying X chromosome-linked Kallmann syndrome.";
RL Mech. Dev. 90:89-94(2000).
DR EMBL; AF163310; AAF25779.1; -.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 652 AA; 72581 MW; 07D6D12D35AA1160 CRC64;

Query Match 28.0%; Score 91.5; DB 13; Length 652;
Best Local Similarity 30.3%; Pred. No. 0.00045;
Matches 20; Conservative 6; Mismatches 19; Indels 21; Gaps 2;

QY 3 EPVKGVPVSTKPGSCPIILIRCAMLNPPNR-----CLKDTDCPGIKKCCGSCGM 51
Db 112 EFLRSVMVVKQGDGP-----PPERASGFAAACVEGCEEDGECGQKKCCPNCGGH 161

QY 52 ACFVPQ 57
Db 162 TCQSPK 167
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RESULT 57
Q8WRP2 PRELIMINARY; PRT; 163 AA.
ID Q8WRP2
AC Q8WRP2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYMPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid
RT shrimp.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430074; AAL36893.1; -.
DR InterPro; IPR002221; WAP.
DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SQ SEQUENCE 163 AA; 16134 MW; E8D443481504C26 CRC64;

Query Match 27.8%; Score 91; DB 5; Length 163;
Best Local Similarity 40.0%; Pred. No. 0.00014;
Matches 20; Conservative 4; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCGSC 49
Db 97 AHEP-ETPVGTKILDPCQVRPTCPRFHGPPTTCSNDYKAGLDKCCFDRC 145

RESULT 58
Q8WRP0 PRELIMINARY; PRT; 169 AA.
ID Q8WRP0
AC Q8WRP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYMPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid
RT shrimp.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430076; AAL36895.1; -.
DR InterPro; IPR002221; WAP.
DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SQ SEQUENCE 169 AA; 16575 MW; 7F6E04EEAC88388E CRC64;

Query Match 27.8%; Score 91; DB 5; Length 169;
Best Local Similarity 40.0%; Pred. No. 0.00014;
Matches 20; Conservative 4; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCGSC 49
Db 103 AHEP-ETPVGTKILDPCQVRPTCPRFHGPPTTCSNDYKAGLDKCCFDRC 151

RESULT 59
Q27087 PRELIMINARY; PRT; 475 AA.
ID Q27087
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AC Q27087;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tt52 protein (Fragment).
GN TT52.
OS Trichuris trichiura.
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida; Trichuridae;
OC Trichuris.
OX NCBI_TaxID=36087;
RN [1]
RP SEQUENCE FROM N.A.
RA Drake L., Brooks H., Barker G.C., Bundy D.A.P.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA Brooks H.;
RL Thesis (1997), Department of Biology, Imperial College of Science,
RL Technology and Medicine, University of London, London, U.K.
DR EMBL; X78981; CAA55584.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 9.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRODom; PD001224; WAP; 4.
DR SMART; SM00217; WAP; 9.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 9.
FT NON_TER 1
SQ SEQUENCE 475 AA; 50257 MW; E6785DED01EF1E65 CRC64;

Query Match 27.7%; Score 90.5; DB 5; Length 475;
Best Local Similarity 38.2%; Pred. No. 0.00046;
Matches 21; Conservative 7; Mismatches 24; Indels 3; Gaps 2;

QY 3 EPVKGVP-VSTKPGSCPILLIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVP 56
Db 320 QPVRWPGPNAPKPGSCPSPVGVAVGL--ASFQSQDFDCMGYQKCCITTAGYECTHP 372

RESULT 60
Q8WRN7
ID Q8WRN7 PRELIMINARY; PRT; 141 AA.
AC Q8WRN7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Litopenaeus setiferus (white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=64468;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid
RT shrimp.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430079; AAL36898.1; -.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 141 AA; 14639 MW; FBDD7707548E8597 CRC64;

Query Match 27.5%; Score 90; DB 5; Length 141;
Best Local Similarity 38.9%; Pred. No. 0.00017;
Matches 21; Conservative 3; Mismatches 18; Indels 12; Gaps 3;

QY 3 EPVKGVPVSTKPGSCPILLIRCAMLNPPNRLKDTDCPGIKKCEGSCG 49
Db 77 BP-EAPVGTKPLDCPQVRPTC---PPTRFGGRPVTCSSDYKCGGLDKCCFDRC 125
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RESULT 61
Q9IAR5
ID Q9IAR5 PRELIMINARY; PRT; 178 AA.
AC Q9IAR5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Kall (Fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20054095; PubMed=10585565;
RA Ardouin O., Legouis R., Fasano L., David-Watine B., Korn H.,
RA Hardelin J.P., Petit C.;
RT "Characterization of the two zebrafish orthologues of the KAL-1 gene
RT underlying X chromosome-linked Kallmann syndrome.";
RL Mech. Dev. 90:89-94(2000).
DR EMBL; AF163309; AAF25778.1; -.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
FT NON_TER 1
FT NON_TER 178
SQ SEQUENCE 178 AA; 19950 MW; BD8192BD7B4072AA CRC64;

Query Match 27.4%; Score 89.5; DB 13; Length 178;
Best Local Similarity 31.0%; Pred. No. 0.00024;
Matches 18; Conservative 3; Mismatches 16; Indels 21; Gaps 2;

QY 10 STKPGSCPILLIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVP 56
Db 22 SSRQGDGP-----PPQRATGFAAACVESCSDQHCPSPRKCCSNGCGHTCQPP 69

RESULT 62
Q9JHY4
ID Q9JHY4 PRELIMINARY; PRT; 80 AA.
AC Q9JHY4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Elafin-like protein I (SWAM1 protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Hagiwara K., Hoshi S., Takahashi M., Miki T., Nukiwa T.;
RT "ELM-like proteins.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., Kikuchi T., Endo Y., Huguin, Takahashi M., Xin X.,
RA Hoshi S., Miki M., Inooka N., Tokue Y., Nukiwa T.;
RT "Mouse SWAM1 (single WAP motif protein 1) gene.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276974; AAF86471.1; -.
DR EMBL; AF482009; AAL90747.1; -.
DR HSSP; O46655; 1CJH.
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DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 80 AA; 9237 MW; 9135647ED91F63ED CRC64;

Query Match 26.8%; Score 87.5; DB 11; Length 80;
Best Local Similarity 37.3%; Pred. No. 0.00021;
Matches 19; Conservative 5; Mismatches 26; Indels 1; Gaps 1;

QY 6 KGPVSTKPGSCPILIRCAMLNPPNRCLKDTDCPGIKKCCGSGCMACFVP 56
| : ||| : : : : : : : : : : : : : : : : : : : : : :
Db 26 KKNVFSKPGYCPYRVPFVLIP-KCRRDKGCKDALKCCFFYQMRCDVP 75

RESULT 63
Q8WS93 PRELIMINARY; PRT; 472 AA.
AC Q8WS93;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KAL-1.
GN KAL-1.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Rugarli E.I., Di Schiavi E., Ghezzi C., Ballabio A., Bazzicalupo P.;
RT "Invertebrate homologs of the Kallmann syndrome gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342987; AAL73339.1; -.
DR InterPro; IPR003962; FNIII_repeat.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SQ SEQUENCE 472 AA; 53942 MW; C80E59470A99DB8E CRC64;

Query Match 26.0%; Score 85; DB 5; Length 472;
Best Local Similarity 30.8%; Pred. No. 0.0025;
Matches 16; Conservative 5; Mismatches 17; Indels 14; Gaps 2;

QY 12 KPGSCPIILIRCAMLNPP-----NRCLKDTDCPGIKKCCGSGCMACFVP 56
| : ||| : : : : : : : : : : : : : : : : : : : : : :
Db 67 KPGKCPV-----SDTPKWEAACVQACNSDSQCDGTQRCCHGCGSTCSEP 111

RESULT 64
Q26615 PRELIMINARY; PRT; 1142 AA.
AC Q26615;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cortical granule protein with LDL-receptor-like repeats
DE (Fragment).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE=OVARY;
RX MEDLINE=95154582; PubMed=7851660;
RA Wessel G.M.;
RT "A protein of the sea urchin cortical granules is targeted to the
RT fertilization envelope and contains an LDL-receptor-like motif.";
RL Dev. Biol. 167:388-397(1995).
DR EMBL; U17377; AAA85106.1; -.
DR HSSP; Q07954; 1CR8.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00057; ldl_recept_a; 14.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00192; LDLA; 14.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS01209; LDLRA_1; 9.
DR PROSITE; PS00068; LDLRA_2; 15.
KW Glycoprotein; Receptor.
FT NON_TER 1142 1142
SQ SEQUENCE 1142 AA; 127733 MW; A43043D2C023AB60 CRC64;

Query Match 26.0%; Score 85; DB 5; Length 1142;
Best Local Similarity 30.3%; Pred. No. 0.0059;
Matches 20; Conservative 5; Mismatches 11; Indels 30; Gaps 4;

QY 11 TKPGSCPILIRCAMLNPP-----NRCLKDTDCPGIKKCC--EGSCGMAC 53
| : ||| : : : : : : : : : : : : : : : : : : : : : :
Db 667 TRPGICP-----PQSNFAYGGNNDPGVCVNDNCFQDTDCPEPMKCCAAPSECGLTC 716

QY 54 ---FVP 56
| : |
Db 717 TQVFLP 722

RESULT 65
Q9JHY3 PRELIMINARY; PRT; 85 AA.
AC Q9JHY3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Elafin-like protein II (SWAM2 protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Hagiwara K., Hoshi S., Takahashi M., Miki T., Nukiwa T.;
RT "ELM-like proteins.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Hagiwara K., Kikuchi T., Endo Y., Takahashi M., Xin X., Hoshi S.,
RA Miki M., Inooka N., Tokue Y., Nukiwa T.;
RT "Mouse SWAM2 (single WAP motif protein 2) gene.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276975; AAF86472.1; -.
DR EMBL; AF482010; AAL90748.1; -.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 85 AA; 9559 MW; 653546C95EF54AD7 CRC64;

Query Match 25.5%; Score 83.5; DB 11; Length 85;
Best Local Similarity 36.6%; Pred. No. 0.00078;
Matches 15; Conservative 5; Mismatches 20; Indels 1; Gaps 1;

QY 16 CPIILIRCAMLNPPNRCLKDTDCPGIKKCCGSGCMACFVP 56
```

1

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK018575; BAB31287.1; -.
DR EMBL; AK009971; BAB26621.1; -.
DR MGD; MGI:1915116; 2310058A03Rik.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SQ SEQUENCE 201 AA; 22043 MW; 3D2E166752A4EEE9 CRC64;

Query Match 24.6%; Score 80.5; DB 11; Length 201;
Best Local Similarity 30.4%; Pred. No. 0.0045;
Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;
QY 8 PVSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMAC 53
Db 61 PRTLPPGAC-----QATRCQADSECPHRRRCYNGCAYAC 95

RESULT 70
QY 8 PVSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMAC 53
Db 61 PRTLPPGAC-----QATRCQADSECPHRRRCYNGCAYAC 95
ID Q8R110 PRELIMINARY; PRT; 207 AA.
AC Q8R110;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to WAP four-disulfide core domain 1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025850; AAH25850.1; -.
FT NON TER 1
SQ SEQUENCE 207 AA; 22706 MW; F816A3CB6FF85640 CRC64;

Query Match 24.6%; Score 80.5; DB 11; Length 207;
Best Local Similarity 30.4%; Pred. No. 0.0047;
Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;

QY 8 PVSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMAC 53
Db 58 PRTLPPGAC-----QATRCQADSECPHRRRCYNGCAYAC 92

RESULT 71
QY 8 PVSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMAC 53
Db 58 PRTLPPGAC-----QATRCQADSECPHRRRCYNGCAYAC 92
ID Q9ESH5 PRELIMINARY; PRT; 211 AA.
AC Q9ESH5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prostate stromal protein ps20.
GN WFDC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=20424791; PubMed=10967136;
RA Larsen M., Ressler S.J., Gerdes M.J., Lu B., Byron M., Lawrence J.B.,
RA Rowley D.R.;
RT "The WFDC1 gene encoding ps20 localizes to 16q24, a region of LOH in
RT multiple cancers.";
RL Mamm. Genome 11:767-773(2000).
DR EMBL; AF170446; AAG21086.1; -.
DR EMBL; AF169632; AAG21086.1; JOINED.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SQ SEQUENCE 211 AA; 23079 MW; 605E7E6B0FC64FE5 CRC64;

Query Match 24.6%; Score 80.5; DB 11; Length 211;
Best Local Similarity 30.4%; Pred. No. 0.0048;
Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;

QY 8 PVSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMAC 53
Db 61 PRTLPPGAC-----QATRCQADSECPHRRRCYNGCAYAC 95

RESULT 72
QY 8 PVSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMAC 53
Db 61 PRTLPPGAC-----QATRCQADSECPHRRRCYNGCAYAC 95
ID O16701 PRELIMINARY; PRT; 249 AA.
AC O16701;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 26.1 kDa protein.
GN R12A1.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Pauley A., Andrews S.;
RT "The sequence of C. elegans cosmid R12A1.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016680; AAB66164.1; -.
DR HSSP; P31713; 1SHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
SQ SEQUENCE 249 AA; 26084 MW; B7BC113CCFF2E1DD CRC64;

Query Match 24.5%; Score 80; DB 5; Length 249;
Best Local Similarity 40.5%; Pred. No. 0.0065;
Matches 15; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 9 VSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCC 45
Db 81 INSKSGCPRPLGISVFDNTIGCWMSNCPGIQKCC 117

RESULT 73
Q9HAU1 PRELIMINARY; PRT; 168 AA.
AC Q9HAU1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE PS20 WAP-type four-disulfide core domain protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Ong C.K., Ng C.Y., Lim K.B., Chan T.W.M.G., Huynh H.;
RT "Molecular Cloning and Characterization of the Human PS20 protein in Human Uterus."
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF302109; AAG15263.1; -.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 168 AA; 18146 MW; 089AA8C5B0B9E1A0 CRC64;

Query Match 24.3%; Score 79.5; DB 4; Length 168;
Best Local Similarity 30.4%; Pred. No. 0.0052;
Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;

QY 8 PVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGCGMAC 53
Db 70 PRTLPPGACQAA-----RCQADSECPHRRCCYNGCAYAC 104

RESULT 74
Q9HC57 PRELIMINARY; PRT; 220 AA.
AC Q9HC57;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Prostate stromal protein ps20.
GN WFDC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=20424791; PubMed=10967136;
RA Larsen M., Ressler S.J., Gerdes M.J., Lu B., Byron M., Lawrence J.B.,
RA Rowley D.R.;
RT "The WFDC1 gene encoding ps20 localizes to 16q24, a region of LOH in

RT multiple cancers.";
RL Mamm. Genome 11:767-773(2000).
DR EMBL; AF169631; AAG16647.1; -.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 220 AA; 24004 MW; 8098EB8449F88CBD CRC64;

Query Match 24.3%; Score 79.5; DB 4; Length 220;
Best Local Similarity 30.4%; Pred. No. 0.0068;
Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;

QY 8 PVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGCGMAC 53
Db 70 PRTLPPGACQAA-----RCQADSECPHRRCCYNGCAYAC 104

RESULT 75
Q9BQY6 PRELIMINARY; PRT; 131 AA.
AC Q9BQY6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE DJ461P17.11 (Novel protein with a WAP-type (Whey acidic protein) 'four-disulfide core' domain and a kunitz/bovine pancreatic trypsin inhibitor domain) (Fragment).
DE DJ461P17.11.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark L.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL031663; CAC36264.1; -.
DR HSSP; P05067; 1AAP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
KW NON TER 131
FT SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;

Query Match 23.5%; Score 77; DB 4; Length 131;
Best Local Similarity 38.9%; Pred. No. 0.009;
Matches 21; Conservative 6; Mismatches 21; Indels 6; Gaps 4;

QY 2 QEP--VKGPVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGCGMAC 53
Db 20 QEPGHAEG-ILGRP--CPKIKVECE-VEEIDQCTKPRDCPENMKCCPFSGRKKC 69

Search completed: February 11, 2003, 08:37:38
Job time : 35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 08:36:01 ; Search time 46 Seconds
(without alignments)
119.123 Million cell updates/sec

Title: 09-833799-13B
Perfect score: 327
Sequence: 1 agepvkpvstkgpcpiil.....cpgikkcecgscgmcfvpq 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	117	2 JH0614	elafin precursor -
2	217.5	66.5	139	2 JE0251	trappin-2 - wart h
3	216.5	66.2	115	2 JE0254	trappin-8 - pig
4	201	61.5	153	2 JE0256	trappin-10 - colla
5	181.5	55.5	207	2 JE0250	trappin-1 - wart h
6	179.5	54.9	187	2 I46650	ATPase inhibitor S
7	177.5	54.3	181	2 JE0253	trappin-7 - pig
8	171.5	52.4	61	2 C33429	ATPase inhibitor 3
9	170	52.0	96	2 JE0252	trappin-6 - bovine
10	166	50.8	180	2 JE0257	trappin-11 - hippo
11	165	50.5	115	2 A36113	antileukoproteinas
12	158	48.3	55	2 B35752	caltrin-like prote
13	143	43.7	132	1 TIHUSP	antileukoproteinas
14	135	41.3	114	2 JE0255	trappin-9 - pig
15	117	35.8	2150	2 T32497	hypothetical prote
16	103	31.5	137	1 WYRT	whely acidic protei
17	101.5	31.0	68	2 S07807	WDM1 protein - ra
18	100.5	30.7	676	2 B47222	Kallmann syndrome
19	99.5	30.4	674	2 A47222	Kallmann syndrome
20	97.5	29.8	1428	2 T08852	lustrin A - Califo
21	97	29.7	125	2 S25454	epididymis-specifi
22	96.5	29.5	74	2 S61553	probable proteinas
23	92.5	28.3	662	2 T23271	hypothetical prote
24	92.5	28.3	679	2 A40351	adhesion-type prot
25	92.5	28.3	680	2 S17982	Kallmann syndrome
26	90.5	27.7	117	2 A24178	Whely acidic protei
27	90.5	27.7	478	2 S47040	gene Tt52 protein
28	88	26.9	124	2 I54768	epididymis-specifi
29	85	26.0	1142	2 T30272	hypothetical prote

30	80	24.5	249	2	T32060	hypothetical prote
31	79.5	24.3	134	1	WYMS	whely acidic protei
32	78	23.9	127	2	S01286	whely acidic protei
33	74.5	22.8	110	1	TITTOR	basic proteinase i
34	71	21.7	273	2	B84868	probable endochiti
35	68.5	20.9	181	2	T32690	hypothetical prote
36	67.5	20.6	333	2	T32058	hypothetical prote
37	67	20.5	1360	2	T33922	hypothetical prote
38	66	20.2	224	2	G69107	conserved hypothet
39	66	20.2	2918	2	A54105	fibrillin-2 precur
40	65	19.9	333	2	B45558	epidermal growth f
41	65	19.9	342	2	D45558	epidermal growth f
42	65	19.9	366	2	D45558	epidermal growth f
43	65	19.9	493	2	T01206	cysteine proteinas
44	65	19.9	1700	2	S08167	Balbani ring 3 pr
45	65	19.9	1717	1	A45558	epidermal growth f
46	64	19.6	230	2	A38346	ultra-high-sulfur
47	64	19.6	293	2	T20523	hypothetical prote
48	64	19.6	334	2	T20524	hypothetical prote
49	64	19.6	1296	2	T16859	hypothetical prote
50	63.5	19.4	2119	2	A35650	Sur protein - chic
51	63	19.3	1101	2	T16840	hypothetical prote
52	63	19.3	2907	2	A57278	hypothetical prote
53	62.5	19.1	202	2	S11434	fibrillin-2 precur
54	62.5	19.1	1964	2	T09059	proteinase - bovin
55	62	19.0	71	2	S47577	notch4 - mouse
56	62	19.0	71	2	S39422	metallothionein 20
57	62	19.0	130	1	S12371	metallothionein 20
58	62	19.0	151	2	S60314	spasmolytic protei
59	62	19.0	178	2	T20466	hair keratin cyste
60	62	19.0	442	2	S50062	hypothetical prote
61	61.5	18.8	1106	2	T44598	cell wall glycopro
62	61.5	18.8	1363	2	T43220	hypothetical prote
63	61	18.7	435	2	S40993	insulin-like growt
64	61	18.7	855	2	A45713	hypothetical prote
65	60.5	18.5	59	2	T44147	Env transmembrane
66	60.5	18.5	1077	2	T41146	B3 protein [import
67	60	18.3	30	2	JX0057	probable cysteine-
68	60	18.3	71	2	S47576	trypsin inhibitor
69	60	18.3	71	2	S39420	metallothionein 20
70	60	18.3	71	2	S39421	metallothionein 20
71	60	18.3	4135	2	T42629	tenascin-X - bovin
72	60	18.3	5376	2	T42215	zonadhesin - mouse
73	59.5	18.2	131	2	T25924	hypothetical prote
74	59.5	18.2	177	2	S37650	high-sulfur kerati
75	59.5	18.2	347	2	D96590	hypothetical prote
76	59.5	18.2	621	2	B89451	protein T04G9.2 [i
77	59	18.0	969	2	T23256	hypothetical prote
78	59	18.0	2871	2	A55624	fibrillin-1 precur
79	59	18.0	3566	1	A40701	tenascin-X precurs
80	58.5	17.9	202	2	JC1358	thiol-endopeptidas
81	58.5	17.9	378	2	B59180	Wnt inhibitory fac
82	58.5	17.9	569	2	S42886	collagen - silkwor
83	58.5	17.9	640	2	T19346	hypothetical prote
84	58.5	17.9	661	2	T42754	hypothetical prote
85	58.5	17.9	1297	2	T30274	proteoliasin - se
86	58	17.7	128	1	S12372	spasmolytic protei
87	58	17.7	574	2	B88465	protein B0244.8 [i
88	57.5	17.6	75	2	S17156	metallothionein -
89	57.5	17.6	265	2	T33695	hypothetical prote
90	57.5	17.6	392	2	T27303	hypothetical prote
91	57.5	17.6	770	2	T00204	LDL receptor relat
92	57.5	17.6	972	2	A30363	glycoprotein GP330
93	57.5	17.6	1513	2	T23681	hypothetical prote
94	57.5	17.6	4660	2	T42737	gp330 protein prec
95	57	17.4	245	2	T27780	hypothetical prote
96	57	17.4	641	2	T03095	homeoprotein Sail
97	57	17.4	954	1	S68178	mixed-lineage prot
98	57	17.4	1847	2	T18308	probable vitelloge
99	56.5	17.3	28	2	JX0059	serine proteinase
100	56.5	17.3	61	1	SMHU1B	metallothionein 1B

RESULT 4

JE0256
trappin-10 - collared peccary
C;Species: Tayassu tajacu (collared peccary)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
C;Accession: JE0256
R;Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.
J. Biochem. 124, 491-502, 1998
A;Title: Evolution of the trappin multigene family in the suidae.
A;Reference number: JE0250; MUID:98391820; PMID:9722657
A;Accession: JE0256
A;Molecule type: mRNA
A;Residues: 1-153 <FUR>
A;Cross-references: DDBJ:D50323
C;Superfamily: antileukoproteinase repeat homology
F;107-152/Domain: antileukoproteinase repeat homology <ALP>

Query Match 61.5%; Score 201; DB 2; Length 153;
Best Local Similarity 55.6%; Pred. No. 6e-14;
Matches 35; Conservative 6; Mismatches 14; Indels 8; Gaps 1;

QY 2 QEPVKGVPST-----KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCGSCGMAC 53

Db 89 QDPVKAELAVRRLVLP RRKPGFCPMIKIRCALFNPENRCLTDAGCPGARKCCIGSCGKAC 148

QY 54 FVP 56

Db 149 LNP 151

RESULT 5

JE0250
trappin-1 - wart hog
C;Species: Phacochoerus aethiopicus (wart hog)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
C;Accession: JE0250
R;Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.
J. Biochem. 124, 491-502, 1998
A;Title: Evolution of the trappin multigene family in the suidae.
A;Reference number: JE0250; MUID:98391820; PMID:9722657
A;Accession: JE0250
A;Molecule type: mRNA
A;Residues: 1-207 <FUR>
A;Cross-references: DDBJ:AB003281
C;Superfamily: antileukoproteinase repeat homology
F;162-207/Domain: antileukoproteinase repeat homology <ALP>

Query Match 55.5%; Score 181.5; DB 2; Length 207;
Best Local Similarity 47.6%; Pred. No. 7.8e-12;
Matches 30; Conservative 10; Mismatches 16; Indels 7; Gaps 1;

QY 2 QEPVKGVPVS-----TKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCGSCGMACF 54

Db 145 QDPIKAQPAVQGLLFLSKRGRCPWILLRCPLANPSNKCWRDYDCPGVKKCCGFCGKDCL 204

QY 55 VPQ 57

Db 205 YPK 207

RESULT 6

I46650
ATPase inhibitor SPAI-2 precursor - pig
N;Contains: ATPase inhibitor SPAI-1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46650; I46651; B33429; A33429
R;Kuroki, J.; Hosoya, T.; Itakura, M.; Hirose, S.; Tamechika, I.; Yoshimoto, T.; Ghoneim
J. Biol. Chem. 270, 22428-22433, 1995
A;Title: Cloning, characterization, and tissue distribution of porcine SPAI, a protein w
A;Reference number: I46650; MUID:95403443; PMID:7673229
A;Accession: I46650
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-187 <KUR>

A;Cross-references: GB:D17753; NID:g1054611; PID:g1054612

A;Accession: I46651

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-187 <KU2>

A;Cross-references: GB:D17755; NID:g1054614; PIDN:BAA04603.1; PID:g1054617

R;Araki, K.; Kuroki, J.; Ito, O.; Kuwada, M.; Tachibana, S.

Biochem. Biophys. Res. Commun. 164, 496-502, 1989

A;Title: Novel peptide inhibitor (SPAI) of Na(+), K(+) -ATPase from porcine intestine.

A;Reference number: A33429; MUID:90026425; PMID:2553020

A;Accession: B33429

A;Molecule type: protein

A;Residues: 127-187 <ARA>

A;Experimental source: duodenum

A;Note: this peptide has four disulfide bonds

A;Accession: A33429

A;Molecule type: protein

A;Residues: 139-187 <AR2>

A;Experimental source: duodenum

C;Genetics:

A;Introns: 28/1

C;Superfamily: antileukoproteinase repeat homology

C;Keywords: ATPase inhibitor

F;127-187/Product: ATPase inhibitor SPAI-2 #status experimental <MA2>

F;139-187/Product: ATPase inhibitor SPAI-1 #status experimental <MA1>

F;142-187/Domain: antileukoproteinase repeat homology <ALP>

Query Match 54.9%; Score 179.5; DB 2; Length 187;
Best Local Similarity 49.2%; Pred. No. 1.2e-11;
Matches 31; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

QY 2 QEPVKGPP-----VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCGSCGMACF 54

Db 125 QDPVKAQPAVPGRFLLSKRGHCPRILFRCPPLSNPSNKCWRDYDCPGVKKCCGFCGKDCL 184

QY 55 VPQ 57

Db 185 YPK 187

RESULT 7

JE0253
trappin-7 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: JE0253
R;Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.
J. Biochem. 124, 491-502, 1998
A;Title: Evolution of the trappin multigene family in the suidae.
A;Reference number: JE0250; MUID:98391820; PMID:9722657
A;Accession: JE0253
A;Molecule type: mRNA
A;Residues: 1-181 <FUR>
A;Cross-references: DDBJ:AB003284

Query Match 54.3%; Score 177.5; DB 2; Length 181;
Best Local Similarity 51.7%; Pred. No. 1.8e-11;
Matches 30; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

QY 1 AQEPVKGPP-VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCGSCGMACFVPQ 57

Db 124 AQPPVQGRLLHYKPGLCWPILRCPLPKPPNKCWRDSDHCHPGVMKCCGFCGNECSYPR 181

RESULT 8

C33429
ATPase inhibitor 3 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Feb-1997
C;Accession: C33429
R;Araki, K.; Kuroki, J.; Ito, O.; Kuwada, M.; Tachibana, S.

QY 2 QEPVKGVPSTKFGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMAC 53

A;Molecule type: protein
A;Residues: 26-34,'X',36-42,'X',44-50,'XE',53-55;103-104,'X',106-107 <BOE>
R;Andrews, J.L.; Melrose, J.; Ghosh, P.
Biol. Chem. Hoppe-Seyler 373, 111-118, 1992
A;Title: A comparative study of the low-molecular mass serine proteinase inhibitors of h
A;Reference number: S21664; MUID:92265184; PMID:1586451
A;Accession: S21664
A;Molecule type: protein
A;Residues: 26-34;36-42;46-50;52-54 <AND>
R;Boudier, C.; Bieth, J.G.
Biochem. J. 303, 61-68, 1994
A;Title: Oxidized mucus proteinase inhibitor: a fairly potent neutrophil elastase inhibi
A;Reference number: S50026; MUID:95031986; PMID:7945266
A;Accession: S50026
A;Molecule type: protein

```

RESULT 15
T32497
hypothetical protein C08G9.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C/Accession: T32497
R;Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C08G9.
A;Reference number: Z21179
A;Accession: T32497
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-2150 <GEI>

```


db , 68 PCKTFVNIEVQKAGRCFVNPIQMIAGPCPKDNPCSI DSDCSGTMKCCNNGCIMSMDPE 127

R;Ellerbrock, K.; Pera, I.; Hartung, S.; Ivell, R.
Int. J. Androl. 17, 314-323, 1994

A;Title: Gene expression in the dog epididymis: a model for human epididymal function.
A;Reference number: I54768; MUID:95263175; PMID:7744511

A;Accession: I54768

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-124 <ELL>

A;Cross-references: GB:S77395; NID:g945180; PIDN:AAB34264.1; PID:g945181

C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology

F;76-123/Domain: antileukoproteinase repeat homology <ALP>

Query Match 26.9%; Score 88; DB 2; Length 124;

Best Local Similarity 38.3%; Pred. No. 0.026;

Matches 18; Conservative 7; Mismatches 20; Indels 2; Gaps 2;

QY 12 KPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCGSCG-MACFVP 56

Db 76 KEGSCPQVNTDFPQLGLCQDQCQVDSHCPLGLKCCYNGCGKVCVTP 122

RESULT 29

T30272

hypothetical protein - sea urchin (Strongylocentrotus purpuratus) (fragment)

C;Species: Strongylocentrotus purpuratus (purple urchin)

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C;Accession: T30272

R;Wessel, G.M.

Dev. Biol. 167, 388-397, 1995

A;Title: A protein of the sea urchin cortical granules is targeted to the fertilization

A;Reference number: Z20801; MUID:95154582; PMID:7851660

A;Accession: T30272

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1142 <WES>

A;Cross-references: EMBL:U17377; NID:g596089; PID:g596090; PIDN:AAA85106.1

Query Match 26.0%; Score 85; DB 2; Length 1142;

Best Local Similarity 30.3%; Pred. No. 0.28;

Matches 20; Conservative 5; Mismatches 11; Indels 30; Gaps 4;

QY 11 TKPGSCPIILIRCAMLNPP-----NRCLKDTDCPGIKKCC--EGSCGMAC 53

Db 667 TRPGICP-----PQSNTAYGGNPDGVCDNCFQDTCPEPMKCCAPSECGLTC 716

QY 54 ---FVP 56

Db 717 TQVFLP 722

RESULT 30

T32060

hypothetical protein R12A1.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T32060

R;Pauley, A.; Andrews, S.

submitted to the EMBL Data Library, July 1997

A;Description: The sequence of C. elegans cosmid R12A1.

A;Reference number: Z21118

A;Accession: T32060

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-249 <PAU>

A;Cross-references: EMBL:AF016680; PIDN:AAB66164.1; GSPDB:GN00023; CESP:R12A1.3

A;Experimental source: strain Bristol N2; clone R12A1

C;Genetics:

A;Gene: CESP:R12A1.3

A;Map position: 5

A;Introns: 75/1; 139/1

Query Match 24.5%; Score 80; DB 2; Length 249;

Best Local Similarity 40.5%; Pred. No. 0.29;

Matches 15; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 9 VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCC 45

Db 81 INKSGSCPRLGLGISVFQDNTIGCWMDSNCPGIQKCC 117

RESULT 31

WYMS

whcy acidic protein precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 16-Jun-2000

C;Accession: A93423; B23879; A01227; A92296

R;Hennighausen, L.G.; Sippel, A.E.

Nucleic Acids Res. 10, 2677-2684, 1982

A;Title: Mouse whcy acidic protein is a novel member of the family of 'four-disulfide co

A;Reference number: A93423; MUID:82196900; PMID:6896234

A;Accession: A93423

A;Molecule type: mRNA

A;Residues: 1-134 <HEN>

A;Note: the cDNA codons given for residues 1 (AGT) and 63 (CGT) are inconsistent with the

A;Note: whcy acidic protein and the neurophysins resemble each other in the number and pa

erwise there is little detectable similarity between these proteins

R;Piletz, J.E.; Heinlen, M.; Ganschow, R.E.

J. Biol. Chem. 256, 11509-11516, 1981

A;Title: Biochemical characterization of a novel whcy protein from murine milk.

A;Reference number: A92296; MUID:82052974; PMID:6975276

A;Contents: annotation; composition of tryptic peptides; strain YBR, variant

A;Note: the variant form appears to have one less Cys and one more Arg

A;Note: no phosphate or carbohydrate binding could be detected; however, both cholesterol

R;Campbell, S.M.; Rosen, J.M.; Hennighausen, L.G.; Strech-Jurk, U.; Sippel, A.E.

Nucleic Acids Res. 12, 8685-8697, 1984

A;Title: Comparison of the whcy acidic protein genes of the rat and mouse.

A;Reference number: A94701; MUID:85062841; PMID:6095207

A;Accession: B23879

A;Molecule type: DNA

A;Residues: 1,'S',3-34,'Q',36-62,'V',64-86,'S',88-99,'K',101-134 <CAM>

A;Cross-references: GB:X01157; NID:g55423; PIDN:CAA25604.1; PID:g1213616

C;Comment: This is one of the major protein components in the milk whey; although its fur

described, inhibitory function.

C;Genetics:

A;Introns: 30/1; 75/1; 130/1

C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology

C;Keywords: duplication; milk; proteinase inhibitor

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-134/Product: whcy acidic protein #status predicted <MAT>

F;30-73/Domain: antileukoproteinase repeat homology <ALP1>

F;79-128/Domain: antileukoproteinase repeat homology <ALP2>

Query Match 24.3%; Score 79.5; DB 1; Length 134;

Best Local Similarity 34.5%; Pred. No. 0.21;

Matches 20; Conservative 4; Mismatches 27; Indels 7; Gaps 2;

QY 6 KGPVS---TKPGSCPIILIRCAMLNPP---NRCLKDTDCPGIKKCCGSCGMACFVP 56

Db 70 KTPVNIQVPKAGFCPWNLQTISSTGCPMQIECSSDRECSGNMKCCNVDCVMTCTPP 127

RESULT 32

S01286

whcy acidic protein precursor - rabbit

N;Alternate names: BIP

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999

C;Accession: S01286; S12586; A12539

R;Devino, E.; Hubert, C.; Schaefer, E.; Houdebine, L.M.; Kraehenbuhl, J.P.

Nucleic Acids Res. 16, 8180, 1988

A;Title: Sequence of the rabbit whcy acidic protein cDNA.

A;Reference number: S01286; MUID:88335562; PMID:3419910

A;Accession: S01286

A;Molecule type: mRNA

A;Residues: 1-127 <DEV>

A;Cross-references: EMBL:X07943; NID:g1779; PIDN:CAA30764.1; PID:g1780

C;Genetics:
A;Gene: CESP:T28C12.6
A;Map position: 5
A;Introns: 53/2; 89/3; 117/1; 157/2; 181/1; 244/2; 286/1

Query Match 20.6%; Score 67.5; DB 2; Length 333;
Best Local Similarity 34.0%; Pred. No. 7.2;
Matches 18; Conservative 2; Mismatches 24; Indels 9; Gaps 3;

Qy 6 KGPVSTKP--GSCPIIL---IRCAMLNPPNRLKDTDCPG-----IKKCCGSGC 49
Db 214 QGSCCTNPSQASCPSTVMNINCRKLSVNCNDFDCRGSTTASMCCTGC 266

RESULT 37
T33922
hypothetical protein Y8A9A.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33922
R;Courtney, L.; Langston, Y.; Drone, K.; Mead, K.
submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid Y8A9A.
A;Reference number: Z21439
A;Accession: T33922
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1360 <COU>
A;Cross-references: EMBL:AF125461; PIDN:AAD12852.1; GSPDB:GN00020; CESP:Y8A9A.2
A;Experimental source: strain Bristol N2; clone Y8A9A
C;Genetics:
A;Gene: CESP:Y8A9A.2
A;Map position: 2
A;Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 787/3; 848/2; 944/2; 1044/2; 1

Query Match 20.5%; Score 67; DB 2; Length 1360;
Best Local Similarity 28.3%; Pred. No. 24;
Matches 15; Conservative 8; Mismatches 18; Indels 12; Gaps 3;

Qy 11 TKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCG-----SCGM-ACFVP 56
Db 914 TTGSCPTTCGSCSTVTQKRVCMSPSTCP-----CQGVSSRSVNCGITVCYFP 961

RESULT 38
G69107
conserved hypothetical protein MTH1801 - Methanobacterium thermoautotrophicum (strain De
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
C;Accession: G69107
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69107
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-224 <WTH>
A;Cross-references: GB:AE000934; GB:AE000666; NID:g2622924; PIDN:AAB86267.1; PID:g262293
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1801
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0045

Query Match 20.2%; Score 66; DB 2; Length 224;
Best Local Similarity 37.5%; Pred. No. 7.6;
Matches 21; Conservative 8; Mismatches 15; Indels 12; Gaps 4;

Qy 2 QEPVKGVPSTKPGSCPIILIRCAMLNPPN-RLKDTDCPGIKKCCGSGMACFVP 56
Db 2 KEPVEGLFT-ARTCREYL-KMFNLNPPDLRLILDPCG-----GASSFTP 46

RESULT 39
A54105
fibrillin-2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Aug-2002
C;Accession: A54105; S17063; S31101
R;Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, E.C.; Sanguinetti, C.; Bonadio, J.; Mecham, R.
J. Cell Biol. 124, 855-863, 1994
A;Title: Structure and expression of fibrillin-2, a novel microfibrillar component prefer
A;Reference number: A54105; MUID:94165150; PMID:8120105
A;Accession: A54105
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-2918 <ZHA>
A;Cross-references: GB:U03272
R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.
Nature 352, 330-334, 1991
A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to tw
A;Reference number: S17062; MUID:91304567; PMID:1852206
A;Accession: S17063
A;Molecule type: mRNA
A;Residues: 752-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928 <LEE>
A;Cross-references: EMBL:X62009
R;Milewicz, D.M.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31101
A;Accession: S31101
A;Molecule type: mRNA
A;Residues: 752-1407,'R',1409-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928
A;Cross-references: EMBL:X62009
C;Genetics:
A;Gene: GDB:FBN2
A;Cross-references: GDB:128122; OMIM:121050
A;Map position: 5q23-5q31
C;Superfamily: fibrillin 1; EGF homology
C;Keywords: extracellular protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-2918/Product: fibrillin-2 #status predicted <MAT>
F;1245-1280/Domain: EGF homology <EGF1>
F;1970-2013/Domain: EGF homology <EGF>

Query Match 20.2%; Score 66; DB 2; Length 2918;
Best Local Similarity 32.4%; Pred. No. 53;
Matches 22; Conservative 6; Mismatches 24; Indels 16; Gaps 4;

Qy 3 EPVKGVPSTKPGSCPII--LIRCAMLNPPNRLKDTDCPGIKKCC-----GSC---- 49
Db 2018 ECVALPGSCSPGTCQNLEGSFRC--ICPPGYEVKSENCIDINEDEPNICLFGSCTNTP 2075

Qy 50 -GMACFVP 56
Db 2076 GGFQCLCP 2083

RESULT 40
B45558
epidermal growth factor receptor homolog precursor (splice form 2) - fluke (Schistosoma m
C;Species: Schistosoma mansoni
C;Date: 22-Apr-1993 #sequence_revision 19-May-1994 #text_change 18-Jun-1999
C;Accession: B45558; S27837
R;Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of epi
A;Reference number: A45558; MUID:92365727; PMID:1501637
A;Accession: B45558
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <SHO1>
A;Note: sequence extracted from NCBI backbone (NCBIP:1111130)
R;Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.
submitted to the EMBL Data Library, February 1992

Query Match 19.9%; Score 65; DB 2; Length 366;
Best Local Similarity 31.2%; Pred. No. 14;
Matches 20; Conservative 10; Mismatches 8; Indels

Qy	14	GSCPII	-----LIRCA	MLPPNRCL	--KDTDC	PGIKKC	--CE	---	GSC	49	
			:	:	:	:	:	:	:	:	
			:	:	:	:	:	:	:	:	
			:	:	:	:	:	:	:	:	
Db	212	GSCPVVN	RGYCWGPK	PEMCOKML	KCAN-NPDNY	CLGGRAT	TOPCL	EECLG	CGCET	TRPGNC	270

QY 50 GMAC 53

Db 271 -RAC 273

RESULT 43

101200
cysteine proteinase mir2 (EC 3.4.22.-) - maize
C:Species: Zea mays (maize)

C:\Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:\Accession: T01206
R:\Pechan, T.; Jiang, B.; Ye, L.; Steckler, D.; Luthe, D.S.; Williams, W.P.

submitted to the EMBL Data Library, August 1997
A;Description: cDNA clones encoding cysteine proteinases from corn (Zea mays L) Callus

A;Reference number: Z14270
A;Accession: T01206

A;Status: preliminary: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-493 <PEC>

A;Cross-references: EMBL:AF019146; NID:g2425063; PIDN:AAB88262.1; PID:g2425064

A; Experimental source: strain Mp708; callus
C. Genetic:

A-Gene. mir3

C:Superfamily: papain

C;Keywords: cysteine proteinase; hydrolase
F:188,324,344/Active site: Cys, His, Asn #status predicted

Query Match 19.9%; Score 65; DB 2; Length 493;

Query Match	19.9%;	Score 65;	DB 2;	Length 493;
Best Local Similarity	31.4%;	Pred. No. 18;		
Matches 16;	Conservative	4;	Mismatches 21;	Indels

Ov 4 PVKGPVSTKPGSCPIILTRCAMLNPDNRCTKNTDQDGIKKCC-----EGSC 49
 Best Local Similarity 31.4%; Pred. No. 18;
 Matches 16; Conservative 4; Mismatches 21; Indels 10; Gaps

QY 4 PVKGPVSTKPGSCPILLIRCAMLNPPNRLKDTDCPGIKKCC-----EGSC 49

Db 378 PVKEGPNPPPGPTP-----PSPVKPPNVCNAEYSCPEATTCCVSEYRGKC 42

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840
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QY 50 GMAC 53

271 - PAC 272

6/2 JUN 1977

RESULT 42

D45558

A;Title: The balbiani ring 3 gene in *Chironomus tentans* has a diverged repeat unit. *Dev Biol*. 1997; 188: 135-145.

C;Accession: D45558; S27839

R; Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Cryst. Liq. Cryst., 1990, Vol. 173, No. 1, 1-10.

MOI: Biochem. Parasitol. 53, 17-32, 1992

A:Reference number: A45558: MUID:92365727: PMID:1501637

A;Accession: D45558

1. *Introduction*

Qv 7 GPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCEGSCGMAC 53

A; Reference number:

A:Cross-references: EMBL:Z82265; NID:e1297698; PIDN:CAB05175.1; GSPDB:GN00022; CESP:F02H

u, D.E.; Flise, E.; Galle, R.; George, R.A.; Harris, N.L.; Hoskins, R.A.; Evans-Holm, M.

Query Match 18.7%; Score 61; DB 2; Length 435;
Best Local Similarity 47.6%; Pred. No. 41;
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 32 CLKDTCPCGKCKEGSCGMA 52
Db 106 CTSDEDCPTTFXCYQGCCKLA 126

RESULT 64
A45713
Env transmembrane protein gp43 - human immunodeficiency virus type 2
C:Species: human immunodeficiency virus type 2, HIV-2
C:Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C:Accession: A45713
R;Barnett, S.W.; Quiroga, M.; Werner, A.; Dina, D.; Levy, J.A.
J. Virol. 67, 1006-1014, 1993
A;Title: Distinguishing features of an infectious molecular clone of the highly divergent
A;Reference number: A45713; MUID:93124535; PMID:8419635
A;Accession: A45713
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-855 <BAR>
A;Experimental source: UC1
A;Note: sequence extracted from NCBI backbone (NCBIP:122362)
C;Superfamily: type E retrovirus env polyprotein

Query Match 18.7%; Score 61; DB 2; Length 855;
Best Local Similarity 38.2%; Pred. No. 69;
Matches 13; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

QY 10 STKPGSCPILIRCA--MLNPPNRCCLKDTCPCI 41
Db 123 TTKPITPTTTTKPSNLLNDTSPCIKNDTCPCI 156

RESULT 65
T44147
B3 protein [imported] - human herpesvirus 6 (strain Z29)
C:Species: human herpesvirus 6
A;Variety: strain Z29
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T44147; T44244
R;Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A;Reference number: Z22734; MUID:99412318; PMID:10482553
A;Accession: T44147
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-59 <DOM>
A;Cross-references: EMBL:AF157706; PIDN:AAD49619.1
A;Experimental source: strain Z29; variant B
A;Genetics: GN1
A;Accession: T44244
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-59 <DO2>
A;Cross-references: EMBL:AF157706; PIDN:AAD49687.1
A;Experimental source: strain Z29; variant B
A;Genetics: GN2
C;Genetics: <GN1>
A;Gene: B3
A;Map position: 7349
C;Genetics: <GN2>
A;Gene: B3
A;Map position: 160670

Query Match 18.5%; Score 60.5; DB 2; Length 59;
Best Local Similarity 33.3%; Pred. No. 10;
Matches 13; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

QY 4 PVKGPVSTKPGSCP---IILIRCAMLNPPNRCCLKDTCPC 39

Db 21 PAFNPMRNKIGECTQSHTMCLRAVLLTPHNKKKHTSCP 59

RESULT 66
T41146
probable cysteine-rich transcription regulator - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
C:Accession: T41146
R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21973
A;Accession: T41146
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1077 <HIL>
A;Cross-references: EMBL:AL031907; PIDN:CAA21417.1; GSPDB:GN00068; SPDB:SPCC18.03
A;Experimental source: strain 972h-; cosmid c18
C;Genetics:
A;Gene: SPDB:SPCC18.03
A;Map position: 3
C;Superfamily: RING finger homology
F;193-252/Domain: RING finger homology <RRN>

Query Match 18.5%; Score 60.5; DB 2; Length 1077;
Best Local Similarity 27.3%; Pred. No. 93;
Matches 21; Conservative 7; Mismatches 18; Indels 31; Gaps 5;

QY 8 PVSTKPGSCP-----IILIRCAMLN---PPNRCCLKDTCPCI----- 41
Db 295 PLLCHPGPCPPCTATVEKFCCLCGKESIHARCSNISKVTEPFC--ENVCDLLPCGEHT 352

QY 42 --KKCCGSGCGMACFVP 56
Db 353 CKKRCHSGLCG-ACFEP 368

RESULT 67
JX0057
trypsin inhibitor MCTI-I - balsam pear
C:Species: Momordica charantia (balsam pear, bitter melon)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Mar-1995
C:Accession: JX0057
R;Hara, S.; Makino, J.; Ikenaka, T.
J. Biochem. 105, 88-92, 1989
A;Title: Amino acid sequences and disulfide bridges of serine proteinase inhibitors from
A;Reference number: JX0057; MUID:89291812; PMID:2738047
A;Accession: JX0057
A;Molecule type: protein
A;Residues: 1-30 <HAR>
A;Experimental source: seed
C;Superfamily: squash trypsin inhibitor ITD I
C;Keywords: serine proteinase inhibitor
F;4-21,11-23,17-29/Disulfide bonds: #status predicted

Query Match 18.3%; Score 60; DB 2; Length 30;
Best Local Similarity 38.9%; Pred. No. 6.9;
Matches 14; Conservative 3; Mismatches 9; Indels 10; Gaps 2;

QY 16 CPIILIRCAMLNPPNRCCLKDTCPCGKKC-CEGSCG 50
Db 4 CPRIL-----KQCKRDSDCPGECICMAHGFCG 30

RESULT 68
S47576
metallothionein 20-Ib - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 17-Mar-1999
C:Accession: S47576
R;Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.;
Eur. J. Biochem. 218, 183-194, 1993

C/Accession: T25924
R/Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A/Description: The sequence of *C. elegans* cosmid T27E4.
A/Reference number: Z20111
A/Accession: T25924
A/Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA
A:Residues: 1-131 <BRA>
A:Cross-references: EMBL:U64837; PIDN:AAB04836.1; GSPDB:GN00023; CESP:T27E4.5
A:Experimental source: strain Bristol N2; clone T27E4
C:Genetics:
A:Gene: CESP:T27E4.5
A:Map position: 5
A:Introns: 40/1; 53/2; 98/1; 118/3

Query Match 18.2%; Score 59.5; DB 2; Length 131;
Best Local Similarity 40.7%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY 32 CLKDTDC--PGIKKCEGSCGM-ACFV 55
| | | | | : | | | | |
Db 80 CKTDQDCMFSNVQKCCDAGCGFNVCV 106

RESULT 74
S37650
high-sulfur keratin - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S37650
R:Zhumabaeva, B.D.; Gening, L.V.; Gazaryan, K.G.
Mol. Biol. 26, 550-555, 1992
A:Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
A:Reference number: S37649
A:Accession: S37650
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <ZHU>
A:Cross-references: EMBL:X63337; NID:g311879; PIDN:CAA44937.1; PID:g311880
C:Superfamily: keratin high-sulfur matrix protein IIIA

Query Match 18.2%; Score 59.5; DB 2; Length 177;
Best Local Similarity 30.4%; Pred. No. 30;
Matches 21; Conservative 7; Mismatches 20; Indels 21; Gaps 6;

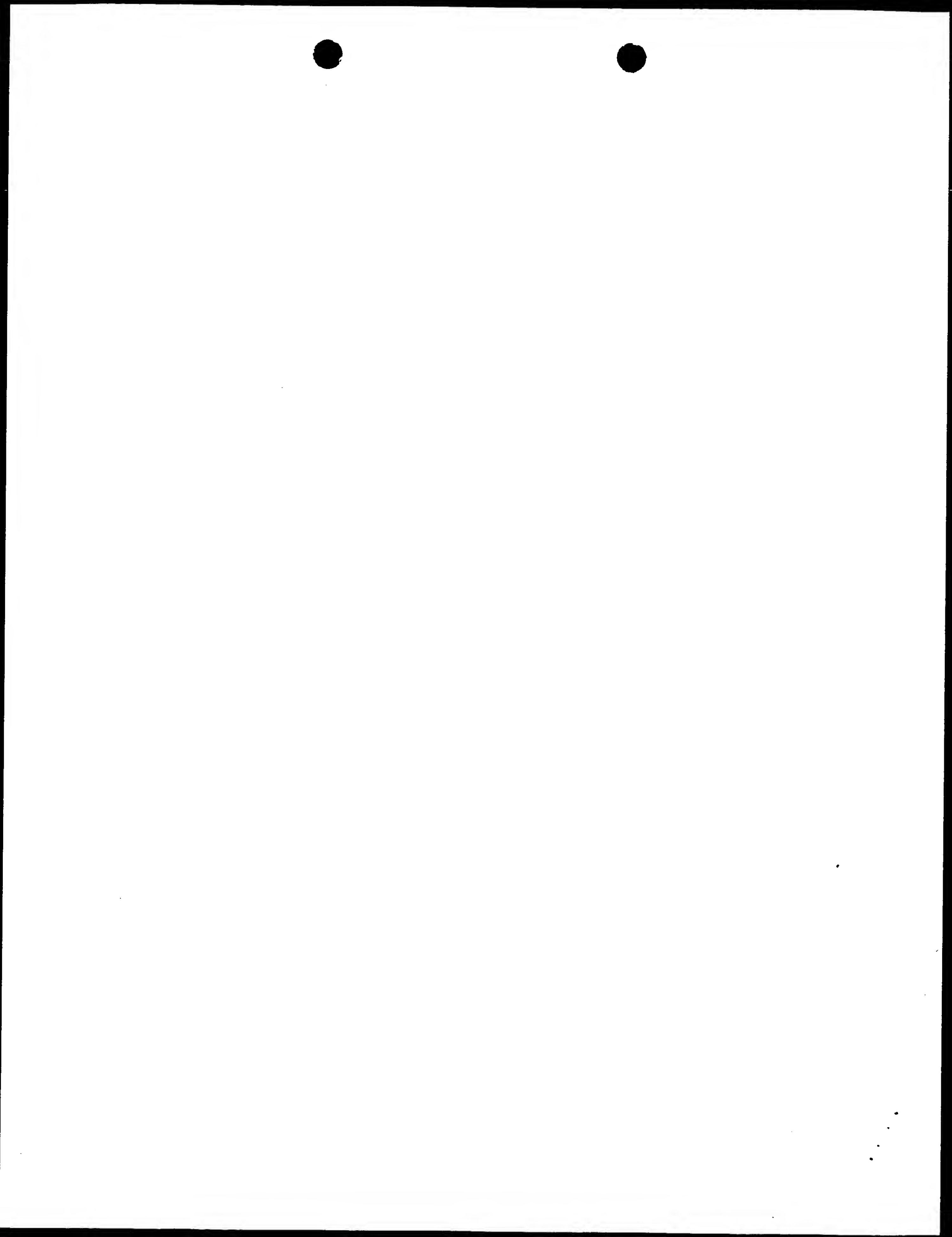
QY 2 QEPVKGPVSTK-----PGSC--PIILIRCAMLNPPNRC-LKDTDCPGIKKCEGS 48
| | | | | : | | | | | : | | | | |
Db 105 QEGSSGAVSTRIRWCRPDCRVEGTCLPPCCVVC---TPPSCCQLHAEAE-----SCCRPS 157

QY 49 -CGMACFVP 56
| | | | |
Db 158 YGQSCCRP 166

RESULT 75
D96590
hypothetical protein T24C10.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96590
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maici, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96590
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <STO>
A:Cross-references: GB:AE005173; NID:g9857516; PIDN:AAG00871.1; GSPDB:GN00141
C:Genetics:
A:Gene: T24C10.2
A:Map position: 1

Query Match 18.2%; Score 59.5; DB 2; Length 347;
Best Local Similarity 30.2%; Pred. No. 50;
Matches 19; Conservative 5; Mismatches 24; Indels 15; Gaps 4;
QY 6 KGPVSTKPGSCPIILIRCAMLNPPN-----RCLKD-----TDCPGIKKCEGSCGMACF 54
| | | | | : | | | | | : | | | | |
Db 39 KSPCFLKKQTCP---KQCPSPFPNGSTKACVIDCFNPICKATCRNRKPNKNGK-GSACL 94
QY 55 VPQ 57
| | | | |
Db 95 DPR 97

Search completed: February 11, 2003, 08:38:52
Job time : 51 secs



GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 21:58:17 ; Search time 47.5 Seconds
(without alignments)
1330.009 Million cell updates/sec

Title: 09-833799-13c

Perfect score: 206

Sequence: 1 gctcgagcattggtatggac.....gcaaggtgtattatcctag 206

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCFUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	32.8	15.9	16950	4	US-09-453-702B-166
C 2	29	14.1	8543	3	US-08-496-944-1
C 3	28.8	14.0	2651	4	US-08-961-527-216
C 4	28.6	13.9	1825	4	US-09-184-964-1
C 5	28.4	13.8	1796	1	US-07-696-551B-11
C 6	28.2	13.7	2007	4	US-08-552-369-7
C 7	28.2	13.7	5009	1	US-08-487-890A-3
C 8	28.2	13.7	5009	2	US-08-478-435-3
C 9	28.2	13.7	5009	2	US-08-337-483-3
10	28.2	13.7	5009	2	US-08-478-373-3
11	28.2	13.7	5009	3	US-08-474-671-3
12	28.2	13.7	5009	3	US-08-483-577A-3
13	28.2	13.7	5009	4	US-08-897-438-3
14	28.2	13.7	5009	4	US-08-637-654-3
15	28.2	13.7	5009	4	US-08-649-518-3
16	28.2	13.7	5033	1	US-08-487-890A-2
17	28.2	13.7	5033	2	US-08-478-435-2
18	28.2	13.7	5033	2	US-08-337-483-2
19	28.2	13.7	5033	2	US-08-478-373-2
20	28.2	13.7	5033	3	US-08-474-671-2
21	28.2	13.7	5033	3	US-08-483-577A-2
22	28.2	13.7	5033	4	US-08-897-438-2
23	28.2	13.7	5033	4	US-08-637-654-2
24	28.2	13.7	5033	4	US-08-649-518-2
C 25	28.2	13.7	6330	4	US-09-880-427-2
C 26	28.2	13.7	6330	4	US-09-306-538B-2
C 27	28	13.6	2007	4	US-08-872-056-23

C 28	28	13.6	162450	4	US-09-345-882-1	Sequence 1, Appli
C 29	27.6	13.4	468	4	US-09-328-111-653	Sequence 653, App
C 30	27.6	13.4	964	1	US-07-798-223A-1	Sequence 1, Appli
C 31	27.2	13.2	4739	4	US-08-677-970-1	Sequence 1, Appli
C 32	27.2	13.2	99500	4	US-09-798-096-10	Sequence 10, Appl
C 33	27.2	13.2	4403765	4	US-09-103-840A-2	Sequence 2, Appli
C 34	26.2	12.7	1797	3	US-08-946-026-13	Sequence 13, Appl
C 35	26.2	12.7	2723	4	US-08-961-527-64	Sequence 64, Appl
C 36	26.2	12.7	4122	4	US-09-321-831-1	Sequence 1, Appli
C 37	26.2	12.7	11873	2	US-08-970-269A-32	Sequence 32, Appl
C 38	26.2	12.7	11873	4	US-09-407-562-32	Sequence 32, Appl
C 39	26.2	12.7	11878	2	US-08-970-269A-31	Sequence 31, Appl
C 40	26.2	12.7	11878	4	US-09-407-562-31	Sequence 31, Appl
C 41	26.2	12.7	11883	2	US-08-970-269A-28	Sequence 28, Appl
C 42	26.2	12.7	11883	4	US-09-407-562-28	Sequence 28, Appl
C 43	26.2	12.7	19250	4	US-08-961-527-35	Sequence 35, Appl
C 44	26	12.6	1550	4	US-09-427-501-1	Sequence 1, Appli
C 45	25.8	12.5	1162	4	US-09-149-476-268	Sequence 268, App
C 46	25.8	12.5	1171	4	US-09-149-476-114	Sequence 114, App
C 47	25.8	12.5	1179	4	US-09-149-476-267	Sequence 267, App
C 48	25.8	12.5	2191	1	US-08-417-330A-11	Sequence 11, Appl
C 49	25.8	12.5	3077	3	US-09-410-028-3	Sequence 3, Appli
C 50	25.6	12.4	3180	2	US-08-500-857A-9	Sequence 9, Appli
C 51	25.6	12.4	5910	1	US-08-195-814-1	Sequence 1, Appli
C 52	25.6	12.4	7620	1	US-07-767-135-1	Sequence 1, Appli
C 53	25.6	12.4	7620	1	US-07-841-652-1	Sequence 1, Appli
C 54	25.6	12.4	65042	4	US-09-784-316-3	Sequence 3, Appli
C 55	25.4	12.3	1632	2	US-08-892-715-1	Sequence 1, Appli
C 56	25.4	12.3	1632	2	US-09-145-947-1	Sequence 1, Appli
C 57	25.4	12.3	1632	4	US-09-265-642-1	Sequence 1, Appli
C 58	25.4	12.3	3097	4	US-09-228-986-11	Sequence 11, Appl
C 59	25.4	12.3	29793	4	US-09-302-812-38	Sequence 38, Appl
C 60	25.4	12.3	29793	4	US-09-511-477-38	Sequence 38, Appl
C 61	25.4	12.3	29793	4	US-09-511-507-38	Sequence 38, Appl
C 62	25.2	12.2	610	1	US-08-425-315-6	Sequence 6, Appli
C 63	25.2	12.2	610	3	US-08-716-190-1	Sequence 1, Appli
C 64	25.2	12.2	1272	4	US-08-908-758-3	Sequence 3, Appli
C 65	25.2	12.2	2169	4	US-09-434-408-3	Sequence 3, Appli
C 66	25	12.1	892	2	US-08-460-529B-1	Sequence 1, Appli
C 67	25	12.1	906	3	US-08-831-132-1	Sequence 1, Appli
C 68	25	12.1	906	4	US-09-416-150-1	Sequence 1, Appli
C 69	25	12.1	1014	4	US-09-134-001C-850	Sequence 850, App
C 70	25	12.1	1665	1	US-08-313-075A-29	Sequence 29, Appl
C 71	25	12.1	1666	1	US-07-912-900-24	Sequence 24, Appl
C 72	25	12.1	1666	1	US-08-285-309-24	Sequence 24, Appl
C 73	25	12.1	1666	2	US-08-502-046-24	Sequence 24, Appl
C 74	25	12.1	1860	1	US-08-624-125-1	Sequence 1, Appli
C 75	25	12.1	2545	1	US-07-869-933-22	Sequence 22, Appl
C 76	25	12.1	2545	4	US-09-103-663-22	Sequence 22, Appl
C 77	25	12.1	3528	4	US-08-984-320-2	Sequence 2, Appli
C 78	25	12.1	3528	4	US-08-487-087A-2	Sequence 2, Appli
C 79	25	12.1	4363	2	US-08-685-576-5	Sequence 5, Appli
C 80	25	12.1	4383	4	US-08-397-653B-2	Sequence 2, Appli
C 81	25	12.1	4383	6	5175095-4	Patent No. 5175095
C 82	25	12.1	4533	3	US-08-863-790-27	Sequence 27, Appl
C 83	25	12.1	4533	3	US-08-296-749-27	Sequence 27, Appl
C 84	25	12.1	4848	4	US-08-961-527-185	Sequence 185, App
C 85	25	12.1	5099	1	US-08-487-890A-4	Sequence 4, Appli
C 86	25	12.1	5099	2	US-08-478-435-4	Sequence 4, Appli
C 87	25	12.1	5099	2	US-08-337-483-4	Sequence 4, Appli
C 88	25	12.1	5099	2	US-08-478-373-4	Sequence 4, Appli
C 89	25	12.1	5099	3	US-08-474-671-4	Sequence 4, Appli
C 90	25	12.1	5099	3	US-08-483-577A-4	Sequence 4, Appli
C 91	25	12.1	5099	4	US-08-897-438-4	Sequence 4, Appli
C 92	25	12.1	5099	4	US-08-637-654-4	Sequence 4, Appli
C 93	25	12.1	5099	4	US-08-649-518-4	Sequence 4, Appli
C 94	25	12.1	7742	2	US-08-882-704A-4	Sequence 4, Appli
C 95	25	12.1	7742	4	US-09-151-957-4	Sequence 4, Appli
C 96	24.8	12.0	666	1	US-08-284-784-23	Sequence 23, Appl
C 97	24.8	12.0	666	2	US-08-854-811-23	Sequence 23, Appl
C 98	24.8	12.0	720	1	US-08-284-784-22	Sequence 22, Appl
C 99	24.8	12.0	720	2	US-08-854-811-22	Sequence 22, Appl
100	24.8	12.0	1010	4	US-09-072-596-316	Sequence 316, App

Patent No. 6040496
GENERAL INFORMATION:
APPLICANT: Law, Marcus D
APPLICANT: Dietz, Jon M
TITLE OF INVENTION: Use of Translationally altered RNA to
TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other
TITLE OF INVENTION: Monocotyledonous Plant Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,944
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1814
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8543 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..8291 /product= "polyprotein encoded by
OTHER INFORMATION: /product= "MDMV-B genome"
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 8292..8530
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 3..1133
OTHER INFORMATION: /product= "3-prime sequence for
OTHER INFORMATION: HC-Pro"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 1134..2375
OTHER INFORMATION: /product= "P3 proteinase"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 2376..4292
OTHER INFORMATION: /product= "cylindrical inclusion
OTHER INFORMATION: protein"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 4293..4451
OTHER INFORMATION: /product= "K2 (6kD protein)"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 4452..5744
OTHER INFORMATION: /product= "Nia proteinase"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 5745..7307
OTHER INFORMATION: /product= "Nib replicase"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 7308..8291

ALIGNMENTS

RESULT 1
US-09-453-702B-166/c
Sequence 166, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
LENGTH: 16950
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-09-453-702B-166
Query Match 15.9%; Score 32.8; DB 4; Length 16950;
Best Local Similarity 50.0%; Pred. No. 0.14;
Matches 82; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 34 TGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAAGCAAC 93
Dbb 13213 TGGCCAAATTTCTGGACGGAGAGAAATATGCTCTGGAAGACCAGCAATAGAAAAACCG 13154
QY 94 GCGATACAATTTGGTGGATTGGCAACAACACTTCCTGTGACTAACAGGTCCATAGTTTTT 153
Dbb 13153 ACAAGATTATGGAGGCGCTTAAGCGTGCAACTACCCATGACTATGAAAGTGTATAGCTTTG 13094
QY 154 CACGACACTTCCAGGACGCCATACCCGACAAAGCAAGGTGTTA 197
Dbb 13093 CTAAAAAATTATCCACAGATGAAGCGATCTGGTAGTTGTGTTA 13050
RESULT 2
US-08-496-944-1/c
Sequence 1, Application US/08496944


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OTHER INFORMATION: /product= "coat protein"
US-08-496-944-1
Query Match 14.1%; Score 29; DB 3; Length 8543;
Best Local Similarity 52.0%; Pred. No. 2.2;
Matches 65; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 14 TATGACGTATACGAGTCTTGGTCAATTTCCAGCACACAGATGATTCGGTCCAAGAAC 73
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1679 TCTGAACACACGCCATATTGCTGAAAATTTTCCACAGTATGACAATTCGCCCATGATTG 1620
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 GGATAATAGAACTAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAACTTCCTGTGA 133
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1619 GTTTAATTGATCTACGTAACATTTTTCATCAGGGTGTATAGGCGTCTCATATAGTGC 1560
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 CTAAC 138
  |||
Db 1559 ATACC 1555

RESULT 3
US-08-961-527-216
; Sequence 216, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-216
Query Match 14.0%; Score 28.8; DB 4; Length 2651;
Best Local Similarity 62.5%; Pred. No. 1.6;
Matches 45; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 99 ACAATTTGGGTGGATGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTCACGA 158
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2357 ACCAAAGGATGTTTGATAAGCTACTTCTCTCTCTAACAATTCCTAGCTTGATCCGA 2416
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 159 CACTTCCAAGGA 170
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Db 2417 CTCTAAGAAGGA 2428
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```
RESULT 4
US-09-184-964-1/c
; Sequence 1, Application US/09184964
; Patent No. 6391574
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper D.
; APPLICANT: Boyartchuk, Victor L.
; APPLICANT: Ashby, Matthew N.
; TITLE OF INVENTION: APC1 AND RCE1: ISOPRENYLATED CAAX
; TITLE OF INVENTION: PROCESSING ENZYMES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill road, suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/184,964
; FILING DATE: 03-NOV-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/902,774
; FILING DATE: 30-JUL-1997
; APPLICATION NUMBER: 60/023,491
; FILING DATE: 07-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Suyat, Reginald J.
; REGISTRATION NUMBER: 28,172
; REFERENCE/DOCKET NUMBER: 09272-006004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/322-5070
; TELEFAX: 650/854-0875
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1825 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
US-09-184-964-1
Query Match 13.9%; Score 28.6; DB 4; Length 1825;
Best Local Similarity 54.2%; Pred. No. 1.6;
Matches 58; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 62 GGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACA 121
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 741 GGTAGACAAACTGGATAAGAGACCCCAAGAGCAATAAACTCTGTGCGACAGTGGAGACCA 682
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 122 AACTTCCTGTGACTAACAGGTCCATAGTTTTCAGCACACTTCCAAG 168
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 681 TATGAAATCTGACTGGCAGGACTGCATTCAATAAAGAAACGGCCATG 635
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-07-696-551B-11/c
; Sequence 11, Application US/07696551B
; Patent No. 5232841
; GENERAL INFORMATION:
; APPLICANT: Hashimoto, Tamotsu
; APPLICANT: Tsujimura, Atsushi
; APPLICANT: Uda, Shigeo
; TITLE OF INVENTION: Process for Preparing Peptide
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
```

Sun Feb 16 09:13:53 2003

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/PC-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/696,551B
FILING DATE: 19910509
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-122166
FILING DATE: 11-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-334575
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence M. Lavin, Jr.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 2481-1070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1796 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-07-696-551B-11
Query Match 13.8%; Score 28.4; DB 1; Length 1796;
Best Local Similarity 58.1%; Pred. No. 1.9;
Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 103 TTTGGGTGGATTGGCAACAACTCTGTGACTAAGAGTCCCATAGTTTTTCCAGCACACT 162
Db 764 TTGGAGTTTATCGGCATCCAGCTTCAAGAGAGACAGCAGTCTTCGTTTTTCTCGAAGCC 705
QY 163 TCCAAGGACGCATACCGAACAAGC 188
Db 704 ACCGATGAAGCCTCTCTGCCGAAGC 679
RESULT 6
US-07-696-551B-11
; Sequence 7, Application US/08552369
; Patent No. 6241989
; GENERAL INFORMATION:
; APPLICANT: Scott, Fred W.
; APPLICANT: Ngichabe, Christopher K.
; APPLICANT: Hu, Liangbiao
; TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
; SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/552,369
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/190,789
FILING DATE: 01/27/1994
APPLICATION NUMBER: 07/726,609
FILING DATE: 07/09/1991
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 18617.0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: yes
ORIGINAL SOURCE:
ORGANISM: feline calicivirus
FEATURE:
LOCATION: capsid protein gene region
US-08-552-369-7
Query Match 13.7%; Score 28.2; DB 4; Length 2007;
Best Local Similarity 54.3%; Pred. No. 2.3;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 55 ATGATTGGTCCAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATT 114
Db 126 AGGATAACAACACACATTAAAGGGTTATCGCAGAACCAACATGTAGAAATTTGTTGGGGTT 67
QY 115 GGCAACAAACTTCTGTGACTAAGAGTCCCATAGTTTTCACGAC 159
Db 66 GATTACCAATTGTGATGTGAGGATCCCAATCATAGTATTAAAGCAC 22
RESULT 7
US-08-487-890A-3
; Sequence 3, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,890A
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 435

```

RESULT 8
US-08-478-435-3
; Sequence 3, Application US/08478435
; Patent No. 5922323
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,435
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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RESULT 9
 US-08-337-483-3
 ; Sequence 3, Application US/08337483
 ; Patent No. 5922562
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena
 ; APPLICANT: Harkness, Robin
 ; APPLICANT: Schryvers, Anthony
 ; APPLICANT: Chong, Pele
 ; APPLICANT: Gray-Owen, Scott
 ; APPLICANT: Yang, Yan-Ping
 ; APPLICANT: Murdin, Andrew
 ; APPLICANT: Klein, Michel
 ; TITLE OF INVENTION: Transferrin Receptor Genes
 ; NUMBER OF SEQUENCES: 147
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sim & McBurney
 ; STREET: Suite 701, 330 Unviersity Avenue
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5G 1R7
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/337,483
 ; FILING DATE: 08-NOV-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stewart, Michael I
 ; REGISTRATION NUMBER: 24,973
 ; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5009 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(121..2100, 2117..4852)
US-08-337-483-3
Query Match 13.7%; Score 28.2; DB 2; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 142 TCCATAGTTTTTCACGACACTTCCAGGAGCGCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1579 TTCTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAACAGGAAGTGCAAAATAT 1638
QY 202 CCTAG 206
Db 1639 CATGG 1643
RESULT 11
US-08-474-671-3
Sequence 3, Application US/08474671
Patent No. 6008326
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,671
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:

TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5009 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(121..2100, 2117..4852)
US-08-337-483-3
Query Match 13.7%; Score 28.2; DB 2; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 142 TCCATAGTTTTTCACGACACTTCCAGGAGCGCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1579 TTCTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAACAGGAAGTGCAAAATAT 1638
QY 202 CCTAG 206
Db 1639 CATGG 1643
RESULT 10
US-08-478-373-3
Sequence 3, Application US/08478373
Patent No. 5922841
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-474-671-3

Query Match      13.7%; Score 28.2; DB 3; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTCACGACACTTCCAAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1579 TTCTTATTAGGTACCGTACTCCCAAGGACGACATACCTAAACACAGGAAGTCAAAATAT 1638

QY 202 CCTAG 206
    |||||
Db 1639 CATGG 1643

RESULT 12
US-08-483-577A-3
; Sequence 3, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-483-577A-3

Query Match      13.7%; Score 28.2; DB 3; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTCACGACACTTCCAAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1579 TTCTTATTAGGTACCGTACTCCCAAGGACGACATACCTAAACACAGGAAGTCAAAATAT 1638

QY 202 CCTAG 206
    |||||
Db 1639 CATGG 1643

RESULT 13
US-08-897-438-3
; Sequence 3, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,438
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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Query Match      13.7%;   Score 28.2;   DB 4;   Length 5009;
Best Local Similarity 64.6%;   Pred. No. 3.4;
Matches 42;   Conservative 0;   Mismatches 23;   Indels 0;   Gaps

QY 142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTATTAT 201
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1579 TTCTTATTAGGTCACCGTACTCTCCAAGGACGACATACCTAAACACAGGAAGTCGCAAAATAT 1638

QY 202 CCTAG 206
    ||| |
Db 1639 CATGG 1643

RESULT 15
US-08-649-518-3
; Sequence 3, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 Unviersity Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,518
; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)

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Matches	42;	Conservative	0;	Mismatches	23;	Indels	0;	Gaps	0;
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Query Match 13.7%; Score 28.2; DB 2; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY	142	TCCATAGTTTTT	CACGACAC	CTTCCA	AGGACGCC	ATACCG	AACA	AAAGCA	AGGTGTTAT	201
Db	1627	TTCTTATTAG	TCACCG	TACTTCCC	AAGACG	CATACCT	TAAAC	CAGGA	AGTGCA	1686
QY	202	CCTAG	206							
Db	1687	CATGG	1691							

RESULT 18
 US-08-337-483-2
 ; Sequence 2, Application US/08337483
 ; Patent No. 5922562
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena
 ; APPLICANT: Harkness, Robin
 ; APPLICANT: Schryvers, Anthony
 ; APPLICANT: Chong, Pele
 ; APPLICANT: Gray-Owen, Scott
 ; APPLICANT: Yang, Yan-ping
 ; APPLICANT: Murdin, Andrew
 ; APPLICANT: Klein, Michel
 ; TITLE OF INVENTION: Transferrin Receptor Genes
 ; NUMBER OF SEQUENCES: 147
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sim & McBurney
 ; STREET: Suite 701, 330 Unviersity Avenue
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(169..2148, 2165..4900)
US-08-337-483-2

Query Match	13.7%;	Score 28.2;	DB 2;	Length 5033;
Best Local Similarity	64.6%;	Pred. No. 3.4;		
Matches	42.	Conservative	0;	Mismatches 23;
				Indels 0;
				Gaps 0;

		TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAGAAGGTCTATTAT	201
QY	142	TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAGAAGGTCTATTAT	201
Dd	1627	TTCTTATTAGGTCA CCGTACTCCC AAGGAC GACATACCTAA ACAGGA AGTGCAA ATAT	1686
QY	202	CCTAG	206
Dd	'1687	CA TGG	1691

RESULT 19
US-08-478-373-2

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; Sequence 2, Application US/08478373
; Patent No. 5922841
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,373
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(169..2148, 2165..4900)
; US-08-478-373-2

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Query Match	13.7%;	Score 28.2;	DB 2;	Length 5033;
Best Local Similarity	64.6%;	Pred. No. 3.4;		
Matches 42. Conservative	0;	Mismatches 23;	Indels 0;	Gaps 0;

	142	1627	202	1687	201
Qy	TCCATAGT	TTCTTATTAGGTC	CCTAG	CATGG	TGTTATTAT
Db	TTCTTATTAGGTC	TTCTTATTAGGTC	CCTAG	CATGG	TGTTATTAT

RESULT 20
US-08-474-671-2
; Sequence 2, Application US/08474671

Patent No. 6008326
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,671
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(169..2148, 2165..4900)
; US-08-474-671-2

Query Match 13.7%; Score 28.2; DB 3; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 142 TCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1627 TTCTTATTAGGTCAACCGTACTCCCAAGGACGACATACCTTAAACACAGGAAGTGCAAAATAT 1686
Qy 202 CCTAG 206
Db 1687 CATGG 1691

RESULT 21
US-08-483-577A-2
; Sequence 2, Application US/08483577A
; Patent No. 6015688

; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(169..2148, 2165..4900)
; US-08-483-577A-2

Query Match 13.7%; Score 28.2; DB 3; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 142 TCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1627 TTCTTATTAGGTCAACCGTACTCCCAAGGACGACATACCTTAAACACAGGAAGTGCAAAATAT 1686
Qy 202 CCTAG 206
Db 1687 CATGG 1691

RESULT 22
US-08-897-438-2
; Sequence 2, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena

; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 Unviersity Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,518
; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(169..2148, 2165..4900)
US-08-649-518-2

Query Match 13.7%; Score 28.2; DB 4; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAGCAAGGTGTTATTAT 201
Db 1627 TTCTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAACACAGGAGTGCAAAATAT 1686
QY 202 CCTAG 206
Db 1687 CATGG 1691

RESULT 25
US-09-880-427-2/c
; Sequence 2, Application US/09880427
; Patent No. 6358728
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hiroyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
;

; FILE REFERENCE: LUD 5601
; CURRENT APPLICATION NUMBER: US/09/880,427
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/306,538
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 6330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5357, 5448
; OTHER INFORMATION: nucleotide not determined
US-09-880-427-2

Query Match 13.7%; Score 28.2; DB 4; Length 6330;
Best Local Similarity 64.6%; Pred. No. 3.7;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 38 CAATTTCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAGCAACGCGA 97
Db 4545 CCACCTGCCCTGGCACAGATGTAGAAATCCAAGTATAGGTTAGGACGACGAGGAAGGGA 4486

QY 98 TACAA 102
Db 4485 TAAAA 4481

RESULT 26
US-09-306-538B-2/c
; Sequence 2, Application US/09306538B
; Patent No. 6372463
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hiroyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
; TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
; FILE REFERENCE: LUD 5601
; CURRENT APPLICATION NUMBER: US/09/306,538B
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 6330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5357, 5448
; OTHER INFORMATION: nucleotide not determined
US-09-306-538B-2

Query Match 13.7%; Score 28.2; DB 4; Length 6330;
Best Local Similarity 64.6%; Pred. No. 3.7;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 38 CAATTTCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAGCAACGCGA 97
Db 4545 CCACCTGCCCTGGCACAGATGTAGAAATCCAAGTATAGGTTAGGACGACGAGGAAGGGA 4486

QY 98 TACAA 102
Db 4485 TAAAA 4481

RESULT 27
US-08-872-056-23/c
; Sequence 23, Application US/08872056
; Patent No. 6231863
; GENERAL INFORMATION:

```

RESULT 28
US-09-345-882-1
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (REP-7)
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```



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; LOCATION: 146345
; OTHER INFORMATION: 5-143-101 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 150329
; OTHER INFORMATION: 5-145-24 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 160031
; OTHER INFORMATION: 5-148-352 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72771..72817
; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72771..72817
; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88050..88096
; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88050..88096
; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90819..90865
; OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90819..90865
; OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93690..93736
; OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93690..93736
; OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97099..97145
; OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97099..97145
; OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97130..97177
; OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97130..97177
; OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99075..99121
; OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99075..99121
; OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99094..99140
; OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99094..99140
```

```
; OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
; FEATURE:
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Query Match 13.6%; Score 28; DB 4; Length 162450;
Best Local Similarity 53.7%; Pred. No. 17;

Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```
QY 33 TTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAAGCAA 92
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74432 TTAATCATTTCTCAATAAACGTGAGATCCTGTGAGCATCAGAAAAGGAAAGAA 74491
```

```
QY 93 CGGATACAATTTGGTGGATTGGCAACAACACTTCCTGTGACTAACAG 140
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74492 GAGTATCTAATTTTAGTAGGTAGGAGAAAATGTAATTTCTAAATAG 74539
```

RESULT 29

US-09-328-111-653/c

; Sequence 653, Application US/09328111

; Patent No. 6262333

; GENERAL INFORMATION:

; APPLICANT: Endege, Willson O.

; APPLICANT: Steinmann, Kathleen E.

; APPLICANT: Astle, Jon H.

; APPLICANT: Burgess, Christopher C.

; APPLICANT: Bushnell, Steven E.

; APPLICANT: Carroll III, Eddie

; APPLICANT: Catino, Theodore J.

; APPLICANT: Derti, Adnan

; APPLICANT: Ford, Donna M.

; APPLICANT: Lewis, Marcia E.

; APPLICANT: Monahan, John E.

; APPLICANT: Schlegel, Robert

; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

; FILE REFERENCE: CCD-257 (US)

; CURRENT APPLICATION NUMBER: US/09/328,111

; CURRENT FILING DATE: 1999-06-08

; EARLIER APPLICATION NUMBER: US 60/088,801

; EARLIER FILING DATE: 1998-06-10

; NUMBER OF SEQ ID NOS: 850

Sun Feb 16 09:13:53 2003

```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 653
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-653

Query Match      13.4%; Score 27.6; DB 4; Length 468;
Best Local Similarity 55.1%; Pred. No. 2;
Matches 54; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 34 TGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAAC 93
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 264 TGATCCATTGGCAACAGGAATCATGACATTAAGAAAATAGTAAAGAAAAATTAGCTAC 205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 94 GCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGT 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 204 CATCTACAGTTTGGTAGCATTGTGACCAATAATTAGGGT 167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 30
US-07-798-223A-1
; Sequence 1, Application US/07798223A
; Patent No. 5422108
; GENERAL INFORMATION:
; APPLICANT: Mirkov, T. Erik
; APPLICANT: Fitzmaurice, Leona Claire
; TITLE OF INVENTION: Protection of Plants Against Pathogens
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/798,223A
; FILING DATE: 19911125
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762,679
; FILING DATE: 19-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 51984
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 964 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 25..459
US-07-798-223A-1

Query Match      13.4%; Score 27.6; DB 1; Length 964;
Best Local Similarity 58.5%; Pred. No. 2.7;
Matches 48; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 69 GAACAGGATAATAGAACTAAGCAACGGATACAATTTGGGTGGATTGGCAACAACTTCC 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 358 GCAAAGCATATTGTCAGTGAGCAAGGCATTACAGCTGGTGGCATGGAATACTATTGT 417

QY 129 TGTGACTAAACAGGTCCATAGTT 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 CGAGACCATGACGTCAGCAGTT 439
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 31
US-08-677-970-1/c
; Sequence 1, Application US/08677970
; Patent No. 644444
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: GENES ENCODING MYCOBACTERIAL PROTEINS
; TITLE OF INVENTION: ASSOCIATED WITH CELL BINDING AND CELL ENTRY AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,970
; FILING DATE: 10-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-592 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4739 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-677-970-1
```

```
Query Match      13.2%; Score 27.2; DB 4; Length 4739;
Best Local Similarity 56.8%; Pred. No. 7.4;
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 95 CGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAAACAGGTCCATAGTTTTC 154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 146 CGTTACAATTTCTGTCGATTTTCCCTTCTCTCCGTGAAACCCAGCTGATGCAGAACGTCTT 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 155 ACGACACTTCCAAGGACGCCATACCGAA 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 TCAACATTCAACAGGCGCGTAGCGCA 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 32
US-09-798-096-10/c
; Sequence 10, Application US/09798096
; Patent No. 6399378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF REQL2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
```


09-833799-13c.rni

Sun Feb 16 09:13:53 2003

```

; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-64

Query Match 12.7%; Score 26.2; DB 4; Length 2723;
Best Local Similarity 53.4%; Pred. No. 13;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 99 ACAATTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTCACGA 158
Db 1499 ACACCTTTGAAATCTTGGAAAGATAAGTAATGTTTCTAAAAATGCCAAGGTATATTATGG 1440

QY 159 CACTTCCAGGACGCCATACCCGAAACAAAGCAAGGTGTTATTAT 201
Db 1439 GAATAACTATAAATCTATAGAAATCAAGCGACCAAGTATGAT 1397

RESULT 36
US-09-321-831-1/c
; Sequence 1, Application US/09321831
; Patent No. 6262336
; GENERAL INFORMATION:
; APPLICANT: LUBON, Henryk
; APPLICANT: DROHAN, William
; APPLICANT: HENNIGHAUSEN, Lothar
; APPLICANT: VELANDER, William
; TITLE OF INVENTION: Expression of a Heterologous Protein C in Mammary Tissue of Tra
; TITLE OF INVENTION: Animals Using a Long Whey Acidic Protein Promoter
; FILE REFERENCE: 030523/0150
; CURRENT APPLICATION NUMBER: US/09/321,831
; CURRENT FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/184,163
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US 07/943,246
; PRIOR FILING DATE: 1992-09-10
; PRIOR APPLICATION NUMBER: US 07/638,995
; PRIOR FILING DATE: 1991-01-11
; PRIOR APPLICATION NUMBER: PCT/US98/02638
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 08/443,184
; PRIOR FILING DATE: 1995-05-17
; PRIOR APPLICATION NUMBER: US 08/198,068
; PRIOR FILING DATE: 1994-02-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4122
; TYPE: DNA
; ORGANISM: WAP gene promoter fragment from the C57B/6 mouse strain
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (544)..(544)
; OTHER INFORMATION: "n" is unknown
; NAME/KEY: misc feature
; LOCATION: (3377)..(544)
; OTHER INFORMATION: "n" is unknown
; US-09-321-831-1

Query Match 12.7%; Score 26.2; DB 4; Length 4122;
Best Local Similarity 60.6%; Pred. No. 16;
Matches 43; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 78 AATAGAACTAAGCAACGGCATACAAATTTGGTGGATTGGCAACAACTTCCTGTGACTAA 137
Db 966 AACAGGCCAGGAAACCCCTTACAGTCTAGGGGGATTTTTCAGTCATGCTGTGATTTA 907

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QY 138 CAGGTCCATAG 148
Db 906 GAGGTACCCAG 896

RESULT 37
US-08-970-269A-32
; Sequence 32, Application US/08970269A
; Patent No. 5976803
; GENERAL INFORMATION:
; APPLICANT: Kathryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,269A
; FILING DATE: No. 5976803ember 14, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11873 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
; US-08-970-269A-32

Query Match 12.7%; Score 26.2; DB 2; Length 11873;
Best Local Similarity 53.4%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 46 AGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACGGCATACAAATTT 105
Db 10851 AAGACATACAGGTGATACCCATGACCTCCAGATTAGGACTTAATTTGAATGGATTGAAAT 10910

QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAG 148
Db 10911 ACTTTTACCTTGAAGGAACTTCTTTTGAGTAACATGTCACAAG 10953

RESULT 38
US-09-407-562-32
; Sequence 32, Application US/09407562
; Patent No. 6294334
; GENERAL INFORMATION:
; APPLICANT: Kathryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease

```


; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,562
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/970,269
; FILING DATE: No. 6294334ember 14, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11873 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
; US-09-407-562-32

Query Match 12.7%; Score 26.2; DB 4; Length 11873;
Best Local Similarity 53.4%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 46 AGGACACAGATGATTTCGGTCCAAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
Db 10851 AAGACATACCAGGTTCATACCCATGACCTCCAGATTAGGACTAATTGAATGGATTGAAAAAT 10910

QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAG 148
Db 10911 ACTTTACCTTGAAGGAACCTCTTTTGAGTAACATGTCACAAG 10953

RESULT 39
US-09-407-269A-31
; Sequence 31, Application US/08970269A
; Patent No. 5976803
; GENERAL INFORMATION:
; APPLICANT: Kathryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,269A
; FILING DATE: No. 5976803ember 14, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11878 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
; US-08-970-269A-31

Query Match 12.7%; Score 26.2; DB 2; Length 11878;
Best Local Similarity 53.4%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 46 AGGACACAGATGATTTCGGTCCAAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
Db 10856 AAGACATACCAGGTTCATACCCATGACCTCCAGATTAGGACTAATTGAATGGATTGAAAAAT 10915

QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAG 148
Db 10916 ACTTTACCTTGAAGGAACCTCTTTTGAGTAACATGTCACAAG 10958

RESULT 40
US-09-407-562-31
; Sequence 31, Application US/09407562
; Patent No. 6294334
; GENERAL INFORMATION:
; APPLICANT: Kathryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,562
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/970,269
; FILING DATE: No. 6294334ember 14, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423

RESULT 42
US-09-407-562-28
; Sequence 28, Application US/09407562
; Patent No. 6294334
; GENERAL INFORMATION:
; APPLICANT: Kathryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston

```

; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,562
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/970,269
; APPLICATION NUMBER: 08/970,269
; FILING DATE: No. 6294334ember 14, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1183 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; US-09-407-562-28

```

QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAAGGTCCATAG 148
| | | | | | | | | | | | | | | | | | | | | |
Db 10921 ACTTTACCTTGAAGGAAGTCTTTTGGAGTAACATGTCAAG 10963

RESULT 43
US-08-961-527-35/c
; Sequence 35, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-35

Query Match 12.7%; Score 26.2; DB 4; Length 19250;
Best Local Similarity 56.3%; Pred. No. 30;
Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 49 ACACAGATGATCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTGGG 108
| | | | | | | | | | | | | | | | | | | | | |
Db 4204 AAACAGAAAATACGGGTCAATTTCTGTAAATATTTCTAAACCTGGCATTACCAAGGGC 4145
QY 109 TGGATTGGCAACAACTTCCTGTGACT 135
| | | | | | | | | | | | | | | | | | | | | |
Db 4144 AACATTGGCATCATTTCTAAGTGGGAAT 4118

RESULT 44
US-09-427-501-1/c
; Sequence 1, Application US/09427501
; Patent No. 6403101
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited, Andrew
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-010
; CURRENT APPLICATION NUMBER: US/09/427,501
; CURRENT FILING DATE: 1999-10-26
; EARLIER APPLICATION NUMBER: 60/106,037
; EARLIER FILING DATE: 1998-10-28

; EARLIER APPLICATION NUMBER: 60/154,658
; EARLIER FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1366)
US-09-427-501-1
Query Match 12.6%; Score 26; DB 4; Length 1550;
Best Local Similarity 57.3%; Pred. No. 12;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 122 AACTTCCTGTGACTAAGGTCCATAGTTTTCACGACACTTCCAAGGACGCCATACCGA 181
| | | | | | | | | | | | | | | | | | | | | |
Db 1085 AACGTACTGTGGCAGACCAGTCTCCAGCTTTTCTGAGTCCCCCTAAAGTTCTCTCAATAA 1026
QY 182 ACAAGCAAGGTGTTATTATCC 203
| | | | | | | | | | | | | | | | | | | | | |
Db 1025 ACCAAGTAGGTTTCTTTTCC 1004
RESULT 45
US-09-149-476-268
; Sequence 268, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581

/	EARLIER APPLICATION NUMBER:	60/056,879
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,880
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,894
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,911
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,636
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,874
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,910
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,864
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,631
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,845
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,892
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/057,761
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/047,595
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,599
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,588
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,585
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,586
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,590
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,594
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,589
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,593
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,614
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/043,578
/	EARLIER FILING DATE:	1997-04-11
/	EARLIER APPLICATION NUMBER:	60/043,576
/	EARLIER FILING DATE:	1997-04-11
/	EARLIER APPLICATION NUMBER:	60/047,501
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/043,670
/	EARLIER FILING DATE:	1997-04-11
/	EARLIER APPLICATION NUMBER:	60/056,632
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,664
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,876
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,881
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,909
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,875
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,862
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,887
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,908
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/048,964
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/057,650

[illegible]

US-08-500-857A-9
; Sequence 9, Application US/08500857A
; Patent No. 5912156
; GENERAL INFORMATION:
; APPLICANT: OHATA, SHOZO
; APPLICANT: USAMI, STORU
; APPLICANT: BURNELL, JAMES N
; TITLE OF INVENTION: POLYPEPTIDE HAVING COLD-STABLE PYRUVATE,
; TITLE OF INVENTION: ORTHOPHOSPHATE KINASE ACTIVITY, DNA ENCODING THE SAME
; TITLE OF INVENTION: AND RECOMBINANT VECTOR AND TRANSFORMED PLANTS CONTAINING
; TITLE OF INVENTION: THE DNA
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
; STREET: 8110 GATE HOUSE ROAD SUITE 500 EAST
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,857A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 760-208P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 103-205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3180 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 142..3006
US-08-500-857A-9
Query Match 12.4%; Score 25.6; DB 2; Length 3180;
Best Local Similarity 59.7%; Pred. No. 23;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
Qy 62 GGTCCAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACA 121
Db 3087 GGTGAAATGAACGATGTTTAAACAAACAAACCCATTATATTTGGTTTGGTATGCAATA 3146
Qy 122 AACTTCCTGTGA 133
Db 3147 ATCTACTTTTCA 3158
RESULT 51
US-08-195-814-1/c
; Sequence 1, Application US/08195814
; Patent No. 5547869
; GENERAL INFORMATION:
; APPLICANT: DUMAS, BRUNO; GERVAIS, MONICA;
; APPLICANT: BERGON, MAX; JOURDAN, MIREITTE; JOUSSET,
; APPLICANT: FRANCOISE XAVIERE
; TITLE OF INVENTION: NOVEL PLASMIDS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVENUE

CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,814
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/881,054
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/278,735
FILING DATE: 2-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1029-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5910
TYPE: NUCLEIC ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: DENSOVIRUS
STRAIN: DENSOVIRUS OF JUNONIA
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: LARVAE
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: SPODOPTERA LITTORALIS
CELL LINE:
ORGANELLE:
FEATURE:
LOCATION: 1
OTHER INFORMATION: N IS A OR C OR G OR T,
OTHER INFORMATION: WHEREIN N IS ZERO TO 50 NUCLEOTIDES IN LENGTH
FEATURE:
LOCATION: 1657
OTHER INFORMATION: M IS A OR C
FEATURE:
LOCATION: 5619
OTHER INFORMATION: Y IS C OR T
FEATURE:
LOCATION: 5910
OTHER INFORMATION: N IS A OR C OR G OR T,
OTHER INFORMATION: WHEREIN N IS ZERO TO 130 NUCLEOTIDES IN LENGTH
US-08-195-814-1
Query Match 12.4%; Score 25.6; DB 1; Length 5910;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 40; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 11 TGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGA 70
Db 1151 TGATTAGTAGTGTGACCTCTGTTAAGTGAATTTCCAGGACCAAGATATTTATATCCGGGA 1092
Qy 71 ACAG 74
Db 1091 ACAG 1088
RESULT 52


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/ LOCATION: 1935..2081
/ OTHER INFORMATION: /product= "Exon 4"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 2082..3046
/ OTHER INFORMATION: /function= "Intron 4"
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 3047..3180
/ OTHER INFORMATION: /product= "Exon 5"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 3181..3390
/ OTHER INFORMATION: /function= "Intron 5"
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 3391..3563
/ OTHER INFORMATION: /product= "Exon 6"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 3564..4116
/ OTHER INFORMATION: /function= "Intron 6"
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 4117..4354
/ OTHER INFORMATION: /product= "Exon 7"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 4355..5227
/ OTHER INFORMATION: /function= "Intron 7"
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 5228..5452
/ OTHER INFORMATION: /product= "Exon 8"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 5453..5852
/ OTHER INFORMATION: /function= "Intron 8"
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 5853..6016
/ OTHER INFORMATION: /product= "Exon 9"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 6017..6385
/ OTHER INFORMATION: /function= "Intron 9"
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 6386..6502
/ OTHER INFORMATION: /product= "Exon 10"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 6503..6596
/ OTHER INFORMATION: /function= "Intron 10"
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 6597..7245
/ US-07-841-652-1

Query Match      12.4%;      Score 25.6;  DB
Best Local Similarity 46.6%;  Pred. No. 33;
Matches 82;  Conservative 0;  Mismatches

QY      27  GAGTCTTGGTCAATTTCCAGGACACAGATGATTGCGTCT
           |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      5395  GAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTA

QY      87  AAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAACT
           |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      5455  AAGCCACCCAGTCTCCCTTCCTGCAAGACAGACCTCAG
           |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY      147  AGTTTTCACGACACTTCCAAGGACGCCCATACCGAACAA
           |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Db 5515 AGACTGACAGAGCCCTTCCTGTCCAGCTTCCCCAGCTAGCCTGCCCTTTTGAGC 5570

RESULT 54

US-09-784-316-3/c

; Sequence 3, Application US/09784316

; Patent No. 6461843

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui et al.

; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001139

; CURRENT APPLICATION NUMBER: US/09/784,316

; CURRENT FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 65042

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(65042)

; OTHER INFORMATION: n = A,T,C or G

US-09-784-316-3

Query Match 12.4%; Score 25.6; DB 4; Length 65042;

Best Local Similarity 59.7%; Pred. No. 82;

Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 21 GTATACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATAAT 80

Db 44646 GTAGATAGGCTCAACACAGAGATGCGAGGGGACAGAGGAAATATCAATGAAGTGGAAAT 44587

QY 81 AGAAGTAAGCAA 92

Db 44586 AGAACAATGTAA 44575

RESULT 55

US-08-892-715-1

; Sequence 1, Application US/08892715

; Patent No. 5922853

; GENERAL INFORMATION:

; APPLICANT: HANSBURY, MICHAEL J

; APPLICANT: JACKSON, JEFFREY R

; TITLE OF INVENTION: A HUMAN PELOTA HOMOLOG

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/892,715

; FILING DATE: 15-JUL-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70144

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1632 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-892-715-1

Query Match 12.3%; Score 25.4; DB 2; Length 1632;

Best Local Similarity 64.4%; Pred. No. 20;

Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 99 ACAATTTGGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCCATAGTTTTTCACG 157

Db 918 ACAAGCAGTGAAGACCGACAACTGCTCTCTGGAACCCGGTCCAAATTTCTTCAGG 976

RESULT 56

US-09-145-947-1

; Sequence 1, Application US/09145947

; Patent No. 5925539

; GENERAL INFORMATION:

; APPLICANT: HANSBURY, MICHAEL J

; APPLICANT: JACKSON, JEFFREY R

; TITLE OF INVENTION: A HUMAN PELOTA HOMOLOG

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/145,947

; FILING DATE: 02-SEPT-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/892,715

; FILING DATE: 15-JUL-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70144-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1632 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-145-947-1

Query Match 12.3%; Score 25.4; DB 2; Length 1632;

Best Local Similarity 64.4%; Pred. No. 20;

Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 99 ACAATTTGGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCCATAGTTTTTCACG 157

Db 918 ACAAGCAGTGAAGACCGACAACTGCTCTCTGGAACCCGGTCCAAATTTCTTCAGG 976

RESULT 57
US-09-265-642-1
; Sequence 1, Application US/09265642
; Patent No. 6342584
; GENERAL INFORMATION:
; APPLICANT: JACKSON, JEFFREY R.
; APPLICANT: HANSBURY, MICHAEL J.
; TITLE OF INVENTION: HUMAN PELOTA HOMOLOG
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,642
; FILING DATE: 10-MAR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/145,947
; FILING DATE: 02-SEP-1998
; APPLICATION NUMBER: 08/892,715
; FILING DATE: 15-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70144-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-265-642-1
Query Match 12.3%; Score 25.4; DB 4; Length 1632;
Best Local Similarity 64.4%; Pred. No. 20;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 99 ACAATTGGTGGATTGGCAACAATTCCTGTGACTAACAGGTCCATAGTTTTTCACG 157
Db 918 ACAAGCAGTGAAGACCGACAACTGCTCTGTGAAACCGTCCAAATTTCTTCAGG 976
RESULT 58
US-09-228-986-11/c
; Sequence 11, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11

; LENGTH: 3097
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-11
Query Match 12.3%; Score 25.4; DB 4; Length 3097;
Best Local Similarity 61.2%; Pred. No. 27;
Matches 41; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 25 ACAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGACAGGATAATAGAA 84
Db 3075 ACAAAAACCTTGCTTAATTTCTTGCACAAATGAATATGAATAAAACAGTATCATACAT 3016
QY 85 CTAAGCA 91
Db 3015 TTAAGTA 3009
RESULT 59
US-09-302-812-38/c
; Sequence 38, Application US/09302812B
; Patent No. 6333148
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/302,812B
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,768
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 38
; LENGTH: 29793
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
US-09-302-812-38
Query Match 12.3%; Score 25.4; DB 4; Length 29793;
Best Local Similarity 64.4%; Pred. No. 69;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 30 TTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGACAGGATAATAGAACTAA 88
Db 3695 TTCGTAGTCTTCTCTCTGTAAAGATGATAATGTTCAAGTAATAAAACTATACTAA 3637
RESULT 60
US-09-511-477-38/c
; Sequence 38, Application US/09511477
; Patent No. 6337202
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AME, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE (PARG) EN
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/511,477
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/302,812
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 38
; LENGTH: 29793
; TYPE: DNA

```
; ORGANISM: Caenorhabditis elegans
; FEATURE:
US-09-511-477-38

Query Match      12.3%; Score 25.4; DB 4; Length 29793;
Best Local Similarity 64.4%; Pred. No. 69;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 30 TTCTTGTCATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAA 88
|||||
Db 3695 TTCGTAGTCTTTCTCCTGTGTAAGAGATGATAATGTTCAAGTAATAAAAACTATACTAA 3637

RESULT 61
US-09-511-507-38/c
; Sequence 38, Application US/09511507
; Patent No. 6395543
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AME, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) EN
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/511,507
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/302,812
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 38
; LENGTH: 29793
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
US-09-511-507-38

Query Match      12.3%; Score 25.4; DB 4; Length 29793;
Best Local Similarity 64.4%; Pred. No. 69;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 30 TTCTTGTCATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAA 88
|||||
Db 3695 TTCGTAGTCTTTCTCCTGTGTAAGAGATGATAATGTTCAAGTAATAAAAACTATACTAA 3637

RESULT 62
US-08-425-315-6/c
; Sequence 6, Application US/08425315
; Patent No. 5545820
; GENERAL INFORMATION:
; APPLICANT: Gatehouse, Angharad
; APPLICANT: Hilder, Vaughan
; APPLICANT: Peumans, Willy
; APPLICANT: Hamilton, William
; TITLE OF INVENTION: INSECTICIDAL PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc and Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,315
; FILING DATE:
```

```
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,841
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mills, Demetra J.
; REGISTRATION NUMBER: 34,506
; REFERENCE/DOCKET NUMBER: 266-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX: 82-4425
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Galantus nivalis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..67
; OTHER INFORMATION: /note= "Putative signal peptide"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 68..382
; OTHER INFORMATION: /note= "Putative mature protein"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 383..487
; OTHER INFORMATION: /note= "Putative C-terminal
; OTHER INFORMATION: peptide"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 488..610
; OTHER INFORMATION: /note= "3' untranslated region"
; US-08-425-315-6

Query Match      12.2%; Score 25.2; DB 1; Length 610;
Best Local Similarity 55.8%; Pred. No. 16;
Matches 48; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 9 CATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68
|||||
Db 142 CATGATAAAACATAATTCCTTGGTTGAGAAATTCGCCGCGAGAGAGAGTCTCGCCAGA 83
|||||
QY 69 GAACAGGATAATAGAACTAAGCAACG 94
|||||
Db 82 GTACAGGATATTATTACTCAGGCAAG 57

RESULT 63
US-08-716-190-1/c
; Sequence 1, Application US/08716190
; Patent No. 6006470
; GENERAL INFORMATION:
; APPLICANT: GEOGHEGAN, Irene
; APPLICANT: ROBERTSON, Walter
; APPLICANT: BIRCH, Nicholas
; APPLICANT: GATEHOUSE, Angharad Margaret
; APPLICANT: ROSCOE
; TITLE OF INVENTION: NEMATOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
```

```

; ZIP: 22314
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,190
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PRICE, Robert L
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 266-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Galanthus nivalis
; IMMEDIATE SOURCE:
; CLONE: LECGNA1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..487
; OTHER INFORMATION: /codon_start= 383
; OTHER INFORMATION: /product= "Putative C-termi
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 2..67
; OTHER INFORMATION: /product= "Putative signal
; OTHER INFORMATION: p"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 68..382
; OTHER INFORMATION: /product= "Putative mature
; OTHER INFORMATION: p"
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 488..610
;
; US-08-716-190-1

```

```

Query Match      12.2%;   Score 25.2;   DB 3;   Length 610;
Best Local Similarity 55.8%;   Pred. NO. 16;
Matches 48;   Conservative 0;   Mismatches 38;   Indels 0;   Gaps 0;

```

[illegible]

RESULT 64
US-08-908-758-3
; Sequence 3, Application US/08908758
; Patent No. 6429356
; GENERAL INFORMATION:
; APPLICANT: Calgene, Inc.
; TITLE OF INVENTION: METHODS FOR P
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis

```

; STATE: CA
; COUNTRY: USA
; ZIP: 95616
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: Microsoft Word For Windows 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,758
; FILING DATE: 8-8-97
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,145
; FILING DATE: 8-9-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: 122-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 3 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1272 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
;
; US-08-908-758-3

```

OTHER INFORMATION: /product=
FEATURE:
FEATURE:

	Matches	42;	Conservative	60.0%;	Pred.	No. 21;	Mismatches	0;	Indels	28;	Gaps	0;
QY	101	AATTTGGGTGATTGGCAACAAACTTCCTGTGAGTAAACAGGTCCATAGTTTTCCAGACA	 	 								
Dd	152	AAGTTGGACTGATTGGTCCTGCACCTTCCTTCCACTAACAACTACGGTGTTGGGAAGATG	 	 								
QY	161	CTTCCAAGGA										
Dd	212	AGTTCAAACGA										

```

RESULT 65
US-09-434-408-3/C
; Sequence 3, Application US/09434408
; Patent No. 6440697
; GENERAL INFORMATION:
; APPLICANT: Venezia, Domenick
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: RING FINGER PROTEIN ZAPO3
; FILE REFERENCE: 98-41
; CURRENT APPLICATION NUMBER: US/09/434,408
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 60/108,258
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate polynucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2169)
; OTHER INFORMATION: n = A,T,C or G
US-09-434-408-3

```

```

; FEATURE:
; OTHER INFORMATION: Degenerate polynucleotide sequence of zapop3
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2169)
; OTHER INFORMATION: n = A, T, C or G
US-09-4334-408-3

```

Patent No. 6008322
GENERAL INFORMATION:
APPLICANT: Kuestner, Rolf E.
APPLICANT: Conklin, Darrell C.
APPLICANT: Lok, Si
APPLICANT: Buddle, Michele
APPLICANT: Downey, William
TITLE OF INVENTION: STANNIOCALCIN-2
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2.5
CURRENT APPLICATION DATA:
FILING DATE: 08/08/83
APPLICATION NUMBER: US/08/831,132
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678

```

, INFORMATION FOR SEQ ID NO: 1:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 906 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: cdna
, FEATURE:
, NAME/KEY: sig_peptide
, LOCATION: 1..72
, FEATURE:
, NAME/KEY: mat_peptide
, LOCATION: 73..906
, FEATURE:
, NAME/KEY: CDS
, LOCATION: 1..906
, US-08-831-132-1

```

```

RESULT 68
US-09-416-150-1/c
; Sequence 1, Application US/09416150
; Patent No. 6171822
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; Konklin, Darrell C.
; Lok, Si
; Buddle, Michele
; Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.

```

TITLE OF INVENTION: STANNIOCALCIN-
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics Inc.


```
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 906 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..72
;
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 73..906
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..906
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-416-150-1
```

```
Query Match 12.1%; Score 25; DB 4; Length 906;
Best Local Similarity 69.4%; Pred. No. 22;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
```

```
QY 143 CCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAGCAAG 191
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 227 CAAGAGTTGTTCTCGAAACATTCAACACACGCCACACCCCATCGCCAG 179
```

```
RESULT 69
US-09-134-001C-850/c
; Sequence 850, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 850
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
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```
; NAME/KEY: unsure
; LOCATION: (32)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-850
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```
Query Match 12.1%; Score 25; DB 4; Length 1014;
Best Local Similarity 48.9%; Pred. No. 23;
Matches 67; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
```

```
QY 64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAA 123
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 405 TCTAACATGTGTAGAAATAGCTTGAGCCACTTTTATTAAATTTTAAGTGGGTGTCACAAAAC 346
```

```
QY 124 CTTCTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAAGGACGCCATACCGAAC 183
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 345 AATATATCTCTTGTCTCTCAGTGATTTGACCAATGTCTAATTTGGTCTCCATTCTTAC 286
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```
QY 184 AAAGCAAGGTGTTATTA 200
| | | | | | | |
Db 285 ATGATAAACAGTTAATA 269
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RESULT 70

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US-08-313-075A-29/c
; Sequence 29, Application US/08313075A
; Patent No. 5639870
```

```
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Tanaka, Yoshikazu
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Scully, Scott, Murphy & Presser
```

```
; STREET: 400 Garden City Plaza
```

```
; CITY: Garden City
```

```
; STATE: New York
```

```
; COUNTRY: U.S.A.
```

```
; ZIP: 11530
```

```
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/313,075A
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; FILING DATE: 30-NOV-1994
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; CLASSIFICATION: 800
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: AU PL 1538/92
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; FILING DATE: 27-MAR-1992
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: AU PL 6698/93
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; FILING DATE: 07-JAN-1993
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: AU PCT/AU93/00127
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; FILING DATE: 25-MAR-1993
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; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: DiGiglio, Frank S.
```

```
; REGISTRATION NUMBER: 31,346
```

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; REFERENCE/DOCKET NUMBER: 9433
```

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; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (516) 742-4343
```

```
; TELEFAX: (516) 742-4366
```

```
; TELEX: 230 901 SANS UR
```

```
; INFORMATION FOR SEQ ID NO: 29:
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```
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 1665 base pairs
```

```
; TYPE: nucleic acid
```

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; STRANDEDNESS: single
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; TOPOLOGY: linear
```

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; MOLECULE TYPE: DNA
```


; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2545 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..786
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 46..54
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 55..786
; US-07-869-933-22

Query Match 12.1%; Score 25; DB 1; Length 2545;
Best Local Similarity 53.6%; Pred. No. 34;
Matches 52; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 61 CGGTCCAAGAACAGGATATAGAACTAAGCAACGCCGATACAAATTTGGGTGGATTGGCAAC 120
Db 1347 CTGAGCAACAACCTGTATTAGTGAATATACCCATGAATTAGATAATATGTCCTTTTCATA 1288
QY 121 AAACCTTCCTGTGACTAACACAGGTCCCATAGTTTTTCACG 157
Db 1287 AAGCTTTATGCTCTGAAAAAACCCATTATTATTGAGG 1251

Search completed: February 15, 2003, 23:42:08
Job time : 1755.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 08:36:01 ; Search time 15 Seconds
(without alignments)
111.807 Million cell updates/sec

Title: 09-833799-13B
Perfect score: 327
Sequence: 1 aqepvkvstkgpscpil.....cpgikkccgscgmactvpq 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	327	100.0	57	1	US-08-379-437-2	Sequence 2, Appli
2	324	99.1	57	1	US-08-379-437-4	Sequence 4, Appli
3	323	98.8	57	1	US-08-379-437-6	Sequence 6, Appli
4	323	98.8	57	1	US-08-379-437-8	Sequence 8, Appli
5	321	98.2	57	1	US-08-379-437-1	Sequence 1, Appli
6	249	76.1	42	2	US-08-761-248B-10	Sequence 10, Appli
7	233	71.3	40	4	US-09-326-039-7	Sequence 7, Appli
8	143	43.7	60	3	US-08-483-503A-1	Sequence 1, Appli
9	143	43.7	107	2	US-07-963-538B-4	Sequence 4, Appli
10	143	43.7	132	1	US-08-304-051-21	Sequence 21, Appli
11	143	43.7	132	5	PCT-US95-11445-21	Sequence 1, Appli
12	141	43.1	53	2	US-07-963-538B-1	Sequence 9, Appli
13	136	41.6	42	2	US-08-761-248B-9	Sequence 3, Appli
14	136	41.6	49	2	US-07-963-538B-3	Sequence 2, Appli
15	136	41.6	50	2	US-07-963-538B-2	Sequence 3, Appli
16	135	41.3	60	3	US-08-483-503A-3	Sequence 4, Appli
17	135	41.3	107	3	US-08-483-503A-4	Sequence 1, Appli
18	99	30.3	49	1	US-08-304-051-1	Sequence 1, Appli
19	99	30.3	49	5	PCT-US95-11445-1	Sequence 1, Appli
20	98	30.0	174	4	US-09-724-864-56	Sequence 56, Appli
21	94.5	28.9	72	4	US-09-383-586-38	Sequence 38, Appli
22	92.5	28.3	680	1	US-08-211-430-2	Sequence 2, Appli
23	92.5	28.3	680	3	US-08-761-136-1	Sequence 1, Appli
24	89	27.2	51	2	US-08-761-248B-14	Sequence 14, Appli
25	88	26.9	43	2	US-08-761-248B-13	Sequence 13, Appli
26	85	26.0	133	4	US-09-152-060-75	Sequence 75, Appli
27	84.5	25.8	44	2	US-08-761-248B-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-379-437-2
; Sequence 2, Application US/08379437
; Patent No. 5734014
; GENERAL INFORMATION:
; APPLICANT: ISHIMA, YOSHIKI
; APPLICANT: OKAWA, NORIYUKI
; APPLICANT: YOSHIDA, MASAYA
; APPLICANT: AMAGAYA, SAKAE
; APPLICANT: KAJI, AKIRA
; TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,437
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP PCT/JP93/01133
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-379-437-2

Query Match 100.0%; Score 327; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AQEPVKGVPSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGCGMACFVPQ 57
Db 1 AQEPVKGVPSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGCGMACFVPQ 57

RESULT 2
US-08-379-437-4
; Sequence 4, Application US/08379437
; Patent No. 5734014
; GENERAL INFORMATION:
; APPLICANT: ISHIMA, YOSHIKI
; APPLICANT: OKAWA, NORIYUKI
; APPLICANT: YOSHIDA, MASAYA
; APPLICANT: AMAGAYA, SAKAE

; APPLICANT: KAJI, AKIRA
; TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,437
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP PCT/JP93/01133
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-379-437-4

Query Match 99.1%; Score 324; DB 1; Length 57;
Best Local Similarity 98.2%; Pred. No. 2.8e-28;
Matches 56; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AQEPVKGVPSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGCGMACFVPQ 57
Db 1 AQEPVKGVPSTKPGSCPIILIRCALLNPPNRLKDTDCPGIKKCCGCGMACFVPQ 57

RESULT 3
US-08-379-437-6
; Sequence 6, Application US/08379437
; Patent No. 5734014
; GENERAL INFORMATION:
; APPLICANT: ISHIMA, YOSHIKI
; APPLICANT: OKAWA, NORIYUKI
; APPLICANT: YOSHIDA, MASAYA
; APPLICANT: AMAGAYA, SAKAE
; APPLICANT: KAJI, AKIRA
; TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; TELEPHONE: 703-413-3000

US-08-379-437-1

US-08-379-437-1

1
; CURRENT APPLICATION NUMBER: US/09/326,039

Query Match 43.7%; Score 143; DB 3; Length 60;
Best Local Similarity 48.2%; Pred. No. 7e-09;
Matches 27; Conservative 4; Mismatches 23; Indels

QY 3 BPVKGPVST--KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSGCMACFVP 56
Db 74 DPVDTPNPTRRKPGKCPVTYGCCLMLNPPNFCFCEMDGQCKRDLKCCMGKSCVSP 129

RESULT 11
PCT-US95-11445-21
; Sequence 21, Application PC/TUS9511445
; GENERAL INFORMATION:
; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria,
; APPLICANT: Katherine A.
; TITLE OF INVENTION: Secretory Leukocyte Protease
; TITLE OF INVENTION: Inhibitor as an Inhibitor of Trypsin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word Perfect 3.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11445
; FILING DATE: 11 September 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/304,051
; FILING DATE: 12 SEPTEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: William F. Gray
; REGISTRATION NUMBER: 31018
; REFERENCE/DOCKET NUMBER: MWH 322P1
; TELEPHONE: (203) 937-2712
; TELEFAX: (203) 937-5492
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION:
; DESCRIPTION: - protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Complete amino acid sequence of human SLPI
; NAME/KEY: (antileukoprotease).
; PUBLICATION INFORMATION:
; AUTHORS: Heinzel, R., Appelhans, H., Gassen, G.,
; AUTHORS: Seemuller, U., Machleidt, W., Fritz, H., and Steffens, G.
; TITLE: Molecular cloning and expression of cDNA for
; TITLE: human antileukoprotease from cervix uterus
; JOURNAL: European Journal of Biochemistry
; VOLUME: 160
; PAGES: 61-67
; DATE: 1986
PCT-US95-11445-21
Query Match 43.7%; Score 143; DB 5; Length 132;
Best Local Similarity 48.2%; Pred. No. 1.5e-08;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 BPVKGPVST--KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSGCMACFVP 56
Db 74, DPVDTPNPTRRKPGKCPVTYGCCLMLNPPNFCFCEMDGQCKRDLKCCMGKSCVSP 129

RESULT 12
US-07-963-538B-1
; Sequence 1, Application US/07963538B
; Patent No. 5851983
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, TAKASHI
; APPLICANT: KAMIMURA, TAKASHI
; APPLICANT: MASUDA, KENICHI
; APPLICANT: OKADA, MASAHIRO
; APPLICANT: OHTSUKA, EIKO
; APPLICANT: IMAIZUMI, ATSUSHI
; APPLICANT: WATANABE, KUNIHITO
; APPLICANT: SUGA, TETSUYA
; APPLICANT: MATSUMOTO, YOHICHI
; APPLICANT: TAKEUCHI, AKIKO
; TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
; TITLE OF INVENTION: TECHNOLOGY
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,538B
; FILING DATE: 20-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/843,359
; FILING DATE: 25-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/408,483
; FILING DATE: 22-AUG-1989
; APPLICATION NUMBER: JP 4-212399
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212398
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-355553
; FILING DATE: 24-DEC-1991
; APPLICATION NUMBER: JP 62-330219
; FILING DATE: 28-DEC-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: TEJN-005/02US
; TELEPHONE: 415-843-5070
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-963-538B-1
Query Match 43.1%; Score 141; DB 2; Length 53;
Best Local Similarity 49.0%; Pred. No. 1e-08;


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; Sequence 3, Application US/08483503A
; Patent No. 6017880
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen
; APPLICANT: Wahl, Sharon M.
; APPLICANT: Thompson, Robert C.
; APPLICANT: Dripps, David J.
; TITLE OF INVENTION: INHIBITION OF RETROVIRUS INFECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,503A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,040
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,369
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barker, M. Paul
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 04189.0084-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-483-503A-3

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Query Match 41.3%; Score 135; DB 3; Length 60;
Best Local Similarity 44.6%; Pred. No. 5e-08;
Matches 25; Conservative 4; Mismatches 25; Indels

QY	3	EPVKG	PVST	--	KPGSC	PIIL	IRCAM	LNP	PNR	CLK	DTD	CPGI	KKCC	EGSC	GCMA	CFVP	56
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Dd	2	DPVDT	PNTR	RRFG	KCPV	TYGQC	XXXN	PPNF	CEX	DGQC	KRDL	KCCX	GXGK	SCVSP			57

US-08-483-503A-4

US 00 483 503A-4
; Sequence 4, Application US/08483503A
; Patent No. 6017880

: GENERAL INFORMATION:

APPLICANT: Eisenberg, Stephen
APPLICANT: Wahl, Sharon M.
APPLICANT: Thompson, Robert C.
APPLICANT: Dripps, David J.

```

/ AMERICAN. DISEASES, DAVID U.
;
; TITLE OF INVENTION:  INHIBITION OF RETROVIRUS INFECTION
;
; NUMBER OF SEQUENCES:  4
;
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Finnegan,

ADDRESSEE: Dunner, L

STREET: 1300 I Street

CITY: Washington

Introduction

STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,503A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,040
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,369
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 04189.0084-02000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-503A-4

Query Match 41.3%; Score 135; DB 3; Length 107;
Best Local Similarity 44.6%; Pred. No. 8.9e-08;
Matches 25; Conservative 4; Mismatches 25; Indels 2; Gaps 1;
QY 3 EPVKGPVST--KPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
DB 49 DPVDTNPTRRKPGKCPVTYQGXNPPNFCBXXDQCKRDLKCCXGCGKSCVSP 104

RESULT 18
US-08-304-051-1
Sequence 1, Application US/08304051
Patent No. 5633227
GENERAL INFORMATION:
APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an
TITLE OF INVENTION: Inhibitor of Tryptase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,051
FILING DATE: 12-Sept-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA: No. 5633227e
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFERENCE/DOCKET NUMBER: MWH 322

TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2712
TELEFAX: (203) 937-2795
TELEX: 221949 MILES UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: - Protein
HYPOTHETICAL: Yes
FRAGMENT TYPE: N-terminal fragment
FEATURE:
NAME/KEY: Related to the sequence of the N-terminal domain of
NAME/KEY: human SLPI. In the listed sequence Xaa at position 18 is Arg or Lys.
US-08-304-051-1

Query Match 30.3%; Score 99; DB 1; Length 49;
Best Local Similarity 38.6%; Pred. No. 0.00029;
Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 10 STKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMAC 53
DB 4 SFGAGVCPKSAQCXLRKPKPECQSDWQCPCGKRCCTCGIKC 47

RESULT 19
PCT-US95-11445-1
Sequence 1, Application PC/TUS9511445
GENERAL INFORMATION:
APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria,
APPLICANT: Katherine A.
TITLE OF INVENTION: Secretory Leukocyte Protease
TITLE OF INVENTION: Inhibitor as an inhibitor of Tryptase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11445
FILING DATE: 11 September 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,051
FILING DATE: 12 SEPTEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFERENCE/DOCKET NUMBER: MWH 322P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2712
TELEFAX: (203) 937-5492
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: - Protein
HYPOTHETICAL: Yes
FRAGMENT TYPE: N-terminal fragment

; FEATURE:
; NAME/KEY: Related to the sequence of the N-terminal
; NAME/KEY: domain of human SLPI. In the listed sequence Xaa at position
; NAME/KEY: 18 is Arg or Lys.
PCT-US95-11445-1

Query Match 30.3%; Score 99; DB 5; Length 49;
Best Local Similarity 38.6%; Pred. No. 0.00029;
Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 10 STKPGSCPIILIRCAMLNPRLKDTDCPGIKKCCGSCGMAC 53
Db 4 SFKAGVCPKKSACQXLYKKPEQCSDWQCPGKKRCCPDTCGIKC 47

RESULT 20

US-09-724-864-56
; Sequence 56, Application US/09724864
; Patent No. 6380362

; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Mouse

US-09-724-864-56

Query Match 30.0%; Score 98; DB 4; Length 174;
Best Local Similarity 33.8%; Pred. No. 0.0013;
Matches 25; Conservative 7; Mismatches 18; Indels 24; Gaps 4;

QY 3 EPVKGPVSTKP-----GSCPII-----LIRCAMLNPRLKDTDCPGIKKC 44
Db 105 KPPGGQVSTKPAVTRGLGVREKQGTCPVDIPKLGLC-----EDQCQVDSQCSEGNMKC 159
QY 45 CEGSCG-MACFPVQ 57
Db 160 CRNGCGKMACTTPK 173

RESULT 21

US-09-383-586-38
; Sequence 38, Application US/09383586
; Patent No. 6242419

; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; TITLE OF INVENTION: and methods for their use
; FILE REFERENCE: 11000.1037c1
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Mouse

US-09-383-586-38

Query Match 28.9%; Score 94.5; DB 4; Length 72;
Best Local Similarity 35.8%; Pred. No. 0.0013;
Matches 19; Conservative 3; Mismatches 14; Indels 17; Gaps 2;

QY 12 KPGSCPIILIRCAMLNP-----NRCLKDTDCPGIKKCCGSCGMACFPV 56
Db 27 KPGACP-----KPSPEVGVICVDQSGDSCPGNMKCCSNGHVCVCKTP 70

RESULT 22

US-08-211-430-2
; Sequence 2, Application US/08211430
; Patent No. 5763166

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: NUCLEIC SEQUENCE OF THE GENE ASSOCIATED WITH
; TITLE OF INVENTION: X CHROMOSOME LINKED KALLMANN SYNDROME, CORRESPONDING
; TITLE OF INVENTION: PEPTIDE SEQUENCES, DIAGNOSTIC APPLICATIONS.

; NUMBER OF SEQUENCES: 32

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/211,430

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 680 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; CELL LINE: foetal brain cell

US-08-211-430-2

Query Match 28.3%; Score 92.5; DB 1; Length 680;
Best Local Similarity 34.6%; Pred. No. 0.02;
Matches 18; Conservative 3; Mismatches 20; Indels 11; Gaps 2;

QY 12 KPGSCPI-----LIRCAMLNPRLKDTDCPGIKKCCGSCGMACFPVQ 57
Db 130 KQGDCAPEKASGFAAACV-----ESCEVDNECSGVKRCSCSNGCGHTCQVPK 176

RESULT 23

US-08-761-136-1
; Sequence 1, Application US/08761136
; Patent No. 6121231

; GENERAL INFORMATION:

; APPLICANT: PETIT, CHRISTINE

; APPLICANT: SOUSSI-YANTICOCTAS, NADIA

; APPLICANT: HARDELIN, JEAN-PIERRE

; APPLICANT: SARAILH, CATHERINE

; APPLICANT: ROUGON, GENEVIEVE

; APPLICANT: LEGOUIS, RENAUD

; APPLICANT: ARDOUIN, OLIVIER

; APPLICANT: MAZIE, JEAN-CLAUDE

; TITLE OF INVENTION: USE OF KAL PROTEIN AND TREATMENT WITH

; TITLE OF INVENTION: THE KAL PROTEIN IN TREATMENT OF RETINAL, RENAL, NEUROMAL

; TITLE OF INVENTION: AND NEURAL INJURY

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,136
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-112-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-412-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 680 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-761-136-1

Query Match 28.3%; Score 92.5; DB 3; Length 680;
Best Local Similarity 34.6%; Pred. No. 0.02;
Matches 18; Conservative 3; Mismatches 20; Indels 11; Gaps 2;

QY 12 KPGSCPI-----ILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFVPQ 57
DB 130 KQGDCAPEKASGFAAACV-----ESCEVDNECSGVKKCCSNGCGHTCQVPK 176

RESULT 24

US-08-761-248B-14
; Sequence 14, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-761-248B-13
Query Match 26.9%; Score 88; DB 2; Length 43;
Best Local Similarity 50.0%; Pred. No. 0.0039;
Matches 13; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-761-248B-14

Query Match 27.2%; Score 89; DB 2; Length 51;
Best Local Similarity 39.0%; Pred. No. 0.0036;
Matches 16; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 17 PIILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFVPQ 57
DB 5 PIQIAAGPCPKDNPCSIDSDCSGTMKCKNGCIMSMDPE 45

RESULT 25

US-08-761-248B-13
; Sequence 13, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-761-248B-13

Query Match 26.9%; Score 88; DB 2; Length 43;
Best Local Similarity 50.0%; Pred. No. 0.0039;
Matches 13; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 32 CLKDTPCPGKCKCEGSCGMACFVPQ 57
DB 18 CEVDNECSGVKKCCSNGCGHTCQVPK 43

RESULT 26
US-09-152-060-75

; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1 US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match 26.0%; Score 85; DB 4; Length 133;
Best Local Similarity 40.4%; Pred. No. 0.025;
Matches 21; Conservative 2; Mismatches 25; Indels 4; Gaps 2;
QY 5 VKGPVSTK---PGSCPILIRCAMLPNRLKDTDCPGIKKCCGCGMAC 53
Db 19 VQGPGLDWLPRRCPKIRECE-FQERDVCTKDRQCQDNKKCCVFCGKKC 69

RESULT 27
US-08-761-248B-8
; Sequence 8, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-761-248B-8
Query Match 25.8%; Score 84.5; DB 2; Length 44;
Best Local Similarity 40.0%; Pred. No. 0.0094;
Matches 14; Conservative 4; Mismatches 16; Indels 1; Gaps 1;
QY 22 RCAMLNPPNRLKDTDCPGIKKCCGCGMACFVP 56
Db 8 QCLRYKKP-ECQSDWQCPGKKRCCPDTCGKICLDP 41

RESULT 28
US-08-761-248B-15
; Sequence 15, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-761-248B-15
Query Match 25.5%; Score 83.5; DB 2; Length 42;
Best Local Similarity 40.5%; Pred. No. 0.012;

Matches 15; Conservative 1; Mismatches 14; Indels 7; Gaps 1;

Qy 27 NPPNR-----CLKDTCPIIKKCCGCGMACFVP 56
||| | | | | | | | | | | | | | | | |
Db 4 NPPRSIGTCVELCGDQSCPNIQKCCSNGCGHVCKSP 40

RESULT 29

US-08-761-248B-7
; Sequence 7, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-761-248B-7

Query Match 24.9%; Score 81.5; DB 2; Length 48;
Best Local Similarity 30.4%; Pred. No. 0.022;
Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;

Qy 8 PVSTKPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGCGMAC 53
| : ||:| | | | | | | | | | | | | | | | |
Db 5 PRTLPPGAC-----QATRCQSDSECPHRRCCYNGCAYAC 39

RESULT 30

US-08-761-248B-2
; Sequence 2, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800

; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-761-248B-2

Query Match 24.9%; Score 81.5; DB 2; Length 212;
Best Local Similarity 30.4%; Pred. No. 0.093;
Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;

Qy 8 PVSTKPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGCGMAC 53
| : ||:| | | | | | | | | | | | | | | | |
Db 62 PRTLPPGAC-----QATRCQSDSECPHRRCCYNGCAYAC 96

RESULT 31

US-08-761-248B-6
; Sequence 6, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723

```

; REFERENCE/DOCKET NUMBER: 34012.6
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (713)9513310
;
; TELEFAX: (713)9513314
;
; TELEFAX:
;

```

```

; ; INFORMATION FOR SEQ ID NO: 6:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 212 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
US-08-761-248B-6

```

Query Match	24.9%;	Score 81.5;	DB 2;	Length 212;
Best Local Similarity	30.4%;	Pred. No. 0.093;		
Matches 14; Conservative	6;	Mismatches 15;	Indels 11;	Gaps 1;

Qy	8	PVSTKPGSCPIILRCAMLNPPNRLKDTPGIIKKCEGSCGMAC	53
Db	62	PTLPPGAC-----QATRCQSDSECPHRRCCYNGCAVAC	96

RESULT 32

US-08-761-248B-4
; Sequence 4, Application US/08761248B

```

;         NO: 09-86753
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

```

ADDRESS: Jenkins & Gilchrist
STREET: 1100 Louisiana, Suite 1800
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77002

```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
```

;;
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/761,248BB
;; FILING DATE: 06-DEC-1996
;; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:

NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34012.6
TELECOMMUNICATION INFORMATION:

TELEPHONE: (713)9513310
TELEFAX: (713)9513314
TELEX:

```

; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 220 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
US-08-761-248B-4

```

Query Match	24.3%;	Score 79.5;	DB 2;	Length 220;
Best Local Similarity	30.4%;	Pred. No. 0.16;		
Matches 14;	Conservative 6;	Mismatches 15;	Indels 1	

QY 8, PVSTKPGSCP I I L I R C A M L N P P N R C L K D T D C P G I K K C C E G S C G M A C 53

Db 70 PRTLPFGACQAA-----RCQADSECPHRRRCYNGCAYAC 104

RESULT 33

US-08-162-146-3
; Sequence 3, Application US/08162146
; Patent No. 5965788
; GENERAL INFORMATION:

```

;
; GENETIC INFORMATION:
; APPLICANT: HOUEBINE, Louis-Marie
; APPLICANT: DEVINOV, Eve
; APPLICANT: THEPOT, Dominique
; TITLE OF INVENTION: Production of a Protein of Interest in
; TITLE OF INVENTION: the Milk of a Transgenic Mammalian
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:

```

ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

```

;
;      200007  3100
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;

```

APPLICATION NUMBER: US/08/162,146
FILING DATE: 10-FEB-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA: PCT/FR92/00533
APPLICATION NUMBER: 12-JUN-1992
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/07179
FILING DATE: 12-JUN-1991

;
 ; ATTORNEY/AGENT INFORMATION:
 ;
 ; NAME: WEGNER, Harold C.
 ;
 ; REGISTRATION NUMBER: 25,258

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

```

;
; LENGTH: 127 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;

```

US-08-162-146-3

Query Match 23.9%; Score 78; DB 2; Length 127;
Best Local Similarity 33.3%; Pred. No. 0.13;
Matches 21; Conservative 4; Mismatches 22; Indels

Matches	21;	Conservative	4;	Mismatches	22;	Indels	16;	Gaps	3;
Matches	21;	Conservative	4;	Mismatches	22;	Indels	16;	Gaps	3;

Qy 10 STKPGSC--PIILI-----RCAMLNPP-----NRCLKDTDCPGIKKCCGSCGMAC 53

Db 58 SAAGGSCRTPIIVPTPKAGRCPPWVOAEMI.SQICEELSDCANDIECRGDKKCCESPCAMPY 11

DD	20 CHAGGGS
OY	54 FVP 56

Db 118 LEP 120

RESULT 34

US-09-314-127-3
; Sequence 3, Application US/09314127

Patent No. 6268545
GENERAL INFORMATION:
APPLICANT: HOUDEBINE, Louis-Marie
APPLICANT: DEVINYOY, Eve
APPLICANT: THEPOT, Dominique

;; TITLE OF INVENTION: Production of a Protein of Interest in
;; TITLE OF INVENTION: the Milk of a Transgenic Mammalian

;; NUMBER OF SEQUENCES: 3
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/314,127

;; FILING DATE:

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/162,146

;; FILING DATE:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 91/07179

;; FILING DATE: 12-JUN-1991

;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEGNER, Harold C.

;; REGISTRATION NUMBER: 25,258

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 672-5300

;; TELEFAX: (202) 672-5399

;; TELEX: 904136

;; INFORMATION FOR SEQ ID NO: 3:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 127 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-09-314-127-3

Query Match 23.9%; Score 78; DB 4; Length 127;

Best Local Similarity 33.3%; Pred. No. 0.13;

Matches 21; Conservative 4; Mismatches 22; Indels 16; Gaps 3;

QY 10 STKPGSC--PIILF-----RCAMLNPP-----NRCLKDTDCPGIKKCCGSGCGMAC 53

Db 58 SAAGSCRTPIIVTPKAGRCWPVQAPMLSQLCEELSDCANDIECRGDKKCCFRCAMRY 117

QY 54 FVP 56

Db 118 LEP 120

RESULT 35

US-08-761-248B-12

;; Sequence 12, Application US/08761248B

;; Patent No. 5958735

;; GENERAL INFORMATION:

;; APPLICANT: ROWLEY,, DAVID R.

;; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH

;; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES

;; NUMBER OF SEQUENCES: 15

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Jenkins & Gilchrist

;; STREET: 1100 Louisiana, Suite 1800

;; CITY: Houston

;; STATE: TX

;; COUNTRY: USA

;; ZIP: 77002

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ for Windows Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/761,248B

;; FILING DATE: 06-DEC-1996

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 60/008,348

;; FILING DATE: 07-DEC-1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Turley, Charles P

;; REGISTRATION NUMBER: 35,723

;; REFERENCE/DOCKET NUMBER: 34012.6

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (713)9513310

;; TELEFAX: (713)9513314

;; TELEX:

;; INFORMATION FOR SEQ ID NO: 12:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 44 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; US-08-761-248B-12

Query Match 20.5%; Score 67; DB 2; Length 44;

Best Local Similarity 30.4%; Pred. No. 0.7;

Matches 14; Conservative 5; Mismatches 15; Indels 12; Gaps 1;

QY 8 PVSTKPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGSGCGMAC 53

Db 2 PKTSGPGIC-----LHGCDSDSDCKEGQKCCFCGCGYIC 35

RESULT 36

US-08-155-171B-21

;; Sequence 21, Application US/08155171B

;; Patent No. 5543264

;; GENERAL INFORMATION:

;; APPLICANT: Anderson, Carl W.

;; APPLICANT: Mangel, Walter F.

;; TITLE OF INVENTION: Co-Factor Activated Recombinant

;; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)

;; NUMBER OF SEQUENCES: 45

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

;; STREET: Two Militia Drive

;; CITY: Lexington

;; STATE: Massachusetts

;; COUNTRY: USA

;; ZIP: 02173

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/155,171B

;; FILING DATE: 19-NOV-1993

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/851,217

;; FILING DATE: 13-MAR-1992

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/545,585

;; FILING DATE: 29-JUN-1990

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Granahan, Patricia

;; REGISTRATION NUMBER: 32,227

;; REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617) 861-6240

;; TELEFAX: (617) 861-9540

Qy	23	CAMLNPP----	NRLKDTDCPGIKKCEG----	SCG----	MACFVP	56
				:		
Db	2199	CAMCPSPLVYNHC--	EHGCP--	RLCEGNTSSCGDPS	EGCFCP	2238
				:		

```
RESULT 45
US-09-132-652-2
; Sequence 2, Application US/09132652
; Patent No. 6074832
; GENERAL INFORMATION:
; APPLICANT: Venta, Patrick J
; APPLICANT: Yuzbasiyan-Gurkan, Vilma
; APPLICANT: Schall, William D
; APPLICANT: Brewer, George J
; APPLICANT: Duffendeck, John
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
; FILE REFERENCE: 2115S-001226CPB
; CURRENT APPLICATION NUMBER: US/09/132,652
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/896,449
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-132-652-2

; Query Match      17.7%; Score 58; DB 3; Length 2813;
; Best Local Similarity 40.0%; Pred. No. 3.9e+02;
; Matches 18; Conservative 2; Mismatches 9; Indels 16; Gaps 5;

QY 23 CAMLNPP-----NRCLKDTCPCGIKKCCG-----SCG-----MACFVP 56
||| ||| : : : : : ||| ||| |||
Db 2199 CAMSCPPSLVYNHC--EHGCP---RLCEGNTSSCGDQPSEGCFCP 2238

RESULT 46
5208144-37
; Patent No. 5208144
; APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/396,697
; FILING DATE: 22-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 313,682
; FILING DATE: 22-FEB-1989
; APPLICATION NUMBER: 235,211
; FILING DATE: 23-AUG-1988
; SEQ ID NO: 37
; LENGTH: 726
5208144-37

; Query Match      17.6%; Score 57.5; DB 6; Length 726;
; Best Local Similarity 34.1%; Pred. No. 1.2e+02;
; Matches 14; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 14 GSCPIILIRCAMLNPPNRLKDT-DCPGIKKCCGSCGMAC 53
||| ||| : : : : : ||| ||| |||
Db 276 GTCQPTQFRC-----PDHRCISPLYVCDGDKDCADGSDEAGC 312

RESULT 47
US-08-785-530-3
; Sequence 3, Application US/08785530
; Patent No. 5814480
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
```

```
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,530
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0194 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 386962
US-08-785-530-3

; Query Match      17.3%; Score 56.5; DB 2; Length 61;
; Best Local Similarity 34.1%; Pred. No. 13;
; Matches 15; Conservative 2; Mismatches 16; Indels 11; Gaps 3;

QY 11 TKPGSCPIILIRCAMLNPPNRC-LKDTDCPGIKKCCGSCGMAC 53
||| ||| : : : : : ||| ||| |||
Db 8 TTGGSC-----ACA-----GSCCKECKCTCKKCCSCCPVGC 41

RESULT 48
US-09-123-850-3
; Sequence 3, Application US/09123850
; Patent No. 5955428
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,850
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,530
; FILING DATE:
```

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0194 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 386962

US-09-123-850-3

Query Match 17.3%; Score 56.5; DB 2; Length 61;
Best Local Similarity 34.1%; Pred. No. 13;
Matches 15; Conservative 2; Mismatches 16; Indels 11; Gaps 3;

QY 11 TKPGSCPIILIRCAMLNPPNRC-LKDTDCPGIKKCCGCGMAC 53

Db 8 TTGGSC-----ACA-----GSKCKCKCKTCKKCCSCCPVGC 41

RESULT 49

US-08-369-043-2

Sequence 2, Application US/08369043

Patent No. 5491064

GENERAL INFORMATION:

APPLICANT: Lichy, Jack H

APPLICANT: Howley, Peter M

TITLE OF INVENTION: HTS1-Gene, A Human Tumor Suppressor Gene

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend

STREET: 1 Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/369,043

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/916,762

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 15280-65

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600

TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1137 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-369-043-2

Query Match 17.3%; Score 56.5; DB 1; Length 1137;

Best Local Similarity 25.0%; Pred. No. 2.3e+02;

Matches 14; Conservative 9; Mismatches 32; Indels 1; Gaps 1;

QY 2 QEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCGCGMACFVP 56

Db 78 QNPQDPSPDTSPTCPFKTASFGYLDSPSACKRDTQKESVQGAQDVAGVAACLP 133

RESULT 50

US-08-611-729A-8

Sequence 8, Application US/08611729A

Patent No. 6004924

GENERAL INFORMATION:

APPLICANT: Ish-Horowicz, David

APPLICANT: Henrique, Domingos M.P.

APPLICANT: Lewis, Julian H.

APPLICANT: Myat, Anna M.

APPLICANT: Fleming, Robert J.

APPLICANT: Artavanis-Tsakonas, Spyridon

APPLICANT: Mann, Robert S.

APPLICANT: Gray, Grace E.

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE

TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/611,729A

FILING DATE: 06-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-037

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1257 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-611-729A-8

Query Match

Best Local Similarity 17.3%; Score 56.5; DB 3; Length 1257;

Matches 12; Conservative 6; Mismatches 14; Indels 5; Gaps 2;

QY 4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPG 40

Db 963 PIRNPIE-RPGGHKDVLYQCKNFTPPPR-----RRCPG 994

RESULT 51

US-08-390-882A-2

Sequence 2, Application US/08390882A

Patent No. 5688764

GENERAL INFORMATION:

APPLICANT: Kral, Robert M. Jr.; Krapcho, Karen; Johnson, Janice

TITLE OF INVENTION: Insecticidal Peptides from Spider

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:


```

; ATTORNEY/AGENT INFORMATION:
; NAME: L. CRAIG METCALF
; REGISTRATION NUMBER: 31,398
; REFERENCE/DOCKET NUMBER: 1094.2.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 537-1700
; TELEFAX: (801) 537-1799
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE: no
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Calisoga sp.
; INDIVIDUAL ISOLATE: peptide C
; ORGANELLE: Venom glands
;
US-08-390-882A-3

Query Match 17.1%; Score 56; DB 1; Length 39;
Best Local Similarity 45.0%; Pred. No. 9.4;
Matches 9; Conservative 3; Mismatches 6; Indels 2

QY 38 CPGIKKCCGSCGM--ACFV 55
| | | | | | | | | |
DB 8 CSNSKDCSCGSGIFWTCYL 27

RESULT 53
US-08-911-423-6
; Sequence 6, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 6:

```

```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-6

```

Query Match 17.1%; Score 56; DB 3; Length 228;
Best Local Similarity 25.8%; Pred. No. 54;
Matches 16; Conservative 4; Mismatches 30; Indels

2;

```

QY      2 QEPVKG-----VSTKPGSCPILIRCAMLNPNRCLKDTDCPGIKKCCGSCGM 51
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     20 QRP TGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQP--EFHCGD 77

```

QY	52	AC	53
Dd	78	PC	79

RESULT 54

US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090

```

;
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;

```

ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA

```

; COUNTRY: USA
; ZIP: 94304-1104
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/911,423
;
; FILING DATE: 14-AUG-1997
;
; CLASSIFICATION: 536

```

```

; SEQUENCE INFORMATION: 350
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PS-08-911-423-7

```

Query Match	17.1%;	Score 56;	DB 3;	Length 232;
Best Local Similarity	25.8%;	Pred. No. 55;		
Matches, 16;	Conservative	4;	Mismatches	30; Indels

QY	2	QEPVKGP-----VSTKPGSCPILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGM	51
D8	20	QRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGECCSEWDCMCVQP--BFHCGD	77
QY	52	AC	53
D8	78	PC	79

RESULT 55

US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090

```

/ GENERAL INFORMATION:
/
/ APPLICANT: Gorman, Daniel M.
/ APPLICANT: Randall, Troy D.
/ APPLICANT: Zlotnik, Albert
/
/ TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
/ TITLE OF INVENTION: REAGENTS
/
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/

```

```

; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
;

```

```

;
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/911,423
;
; FILING DATE: 14-AUG-1997
;
;

```

```

; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-911-423-4

```

Query Match 17.1%; Score 56; DB 3; Length 241;
Best Local Similarity 25.8%;
Pred. NO. 57;
Matches 16; Conservative 4; Mismatches 30; Indels 12; Gaps 2;

QY	2	QEPVKG	-----VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCEGSCGM	51
Db	26	QRPTGGPGGGRLLLTGT	DARCCRVHTTRCCRDYPGECCSEWDCMCVQP--EFHCGD	83
QY	52	AC	53	
Db	84	PC	85	

RESULT 56
US-08-937-931-6

```
; Sequence 6, Application US/08937931
; Patent No. 5935792
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 5935792e1 Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,931
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-937-931-6

Query Match 17.1%; Score 56; DB 2; Length 265;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRCLKDTDCPGIKKCEGSC-GMAC 53
Db 184 ANQPEGRKCKLPGKQCSQSPGCTTAQCAFKSKSEKCRDDSDC-----AREGICNGFTA 238

QY 54 FVP 56
Db 239 LCP 241

US-08-937-931-6

RESULT 57
US-09-285-502-6
; Sequence 6, Application US/09285502
; Patent No. 6190876
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6190876e1 Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
```

```
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/937,931
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-285-502-6

Query Match 17.1%; Score 56; DB 4; Length 265;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRCLKDTDCPGIKKCEGSC-GMAC 53
Db 184 ANQPEGRKCKLPGKQCSQSPGCTTAQCAFKSKSEKCRDDSDC-----AREGICNGFTA 238

QY 54 FVP 56
Db 239 LCP 241

US-09-285-502-6

RESULT 58
US-09-709-126-6
; Sequence 6, Application US/09709126
; Patent No. 6319704
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6319704e1 Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/709,126
; FILING DATE: 08-No. 6319704-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,502
; FILING DATE: <Unknown>
```

```
;
;
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-709-126-6

Query Match      17.1%; Score 56; DB 4; Length 265;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRLKDTDCPGIKKCEGSC-GMAC 53
Db 184 ANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDSDC-----AREGICNGFTA 238

QY 54 FVP 56
Db 239 LCP 241

RESULT 59
US-09-871-385A-6
; Sequence 6, Application US/09871385A
; Patent No. 6399350
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; Pan, Duojia
; Rooke, Jenny
; Yavari, Reza
; Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6399350el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,385A
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/709,126
; FILING DATE: 08-No. 6399350-2000
; APPLICATION NUMBER: 09/285,502
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
```

```
;
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-871-385A-6

Query Match      17.1%; Score 56; DB 4; Length 265;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRLKDTDCPGIKKCEGSC-GMAC 53
Db 184 ANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDSDC-----AREGICNGFTA 238

QY 54 FVP 56
Db 239 LCP 241

RESULT 60
US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-911-423-8

Query Match      17.1%; Score 56; DB 3; Length 311;
Best Local Similarity 25.8%; Pred. No. 73;
Matches 16; Conservative 4; Mismatches 30; Indels 12; Gaps 2;
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QY 2 QEPVKGP-----VSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGM 51
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Db 20 QRTGGPGCGPRLLLGTGTDAARCCRVHTTRCCRDYPGEECCSEWDCMCVQP--EFHCGD 77
| | | | | : | | | | | : | | | | | : | | | | |
QY 52 AC 53
| | | | | : | | | | | : | | | | | : | | | | |
Db 78 PC 79
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 61
US-09-030-335-2
; Sequence 2, Application US/09030335
; Patent No. 6255064
; GENERAL INFORMATION:
; APPLICANT: Tindal, Michael H
; APPLICANT: Haqqi, Tariq M
; TITLE OF INVENTION: Use of a No. 6255064el Disintegrin Metalloprotease, Mutants,
; TITLE OF INVENTION: Fragments and the Like
; FILE REFERENCE: Metalloprotease
; CURRENT APPLICATION NUMBER: US/09/030,335
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-030-335-2

Query Match 17.1%; Score 56; DB 4; Length 491;
Best Local Similarity 28.6%; Pred. No. 1.1e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRLKDTDCPGIKKCCGSC-GMAC 53
| | | | | : | | | | | : | | | | | : | | | | |
Db 230 ANQPEGRKCKLKPQKQCSQSPGCTAQCFAFKSKSEKCRDDSDC-----AREGICNGFTA 284
| | | | | : | | | | | : | | | | | : | | | | |
QY 54 FVP 56
| | | | | : | | | | | : | | | | | : | | | | |
Db 285 LCP 287
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 62
US-08-920-234-2
; Sequence 2, Application US/08920234
; Patent No. 5922546
; GENERAL INFORMATION:
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: MAYER, RUTH
; TITLE OF INVENTION: HUMAN DISINTEGRIN METALLOPROTEASE
; TITLE OF INVENTION: RELATED TO DROSOPHILA KUZ GENE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,234
; FILING DATE: 25-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70237
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-920-234-2

Query Match 17.1%; Score 56; DB 2; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;
QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRLKDTDCPGIKKCCGSC-GMAC 53
| | | | | : | | | | | : | | | | | : | | | | |
Db 487 ANQPEGRKCKLKPQKQCSQSPGCTAQCFAFKSKSEKCRDDSDC-----AREGICNGFTA 541
| | | | | : | | | | | : | | | | | : | | | | |
QY 54 FVP 56
| | | | | : | | | | | : | | | | | : | | | | |
Db 542 LCP 544
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 63
US-08-937-931-4
; Sequence 4, Application US/08937931
; Patent No. 5935792
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 5935792el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,931
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-937-931-4

```

Query Match      17.1%; Score 56; DB 2; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRCUKDTDCPGIKKCEGSC-GMAC 53
Db 487 ANQPEGRKCKLPGKQCSPSQGPCCTAQCAFKSKSEKCRDSDC-----AREGICNGFTA 541

QY 54 FVP 56
Db 542 LCP 544

RESULT 64
US-09-285-502-4
; Sequence 4, Application US/09285502
; Patent No. 6190876
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6190876el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,931
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-285-502-4

Query Match      17.1%; Score 56; DB 4; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRCUKDTDCPGIKKCEGSC-GMAC 53
Db 487 ANQPEGRKCKLPGKQCSPSQGPCCTAQCAFKSKSEKCRDSDC-----AREGICNGFTA 541

QY 54 FVP 56
Db 542 LCP 544

```


RESULT 70
US-09-709-126-8
; Sequence 8, Application US/09709126
; Patent No. 6319704
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; Pan, Duoqia
; Rooke, Jenny
; Yavari, Reza
; Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6319704el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA

APPLICATION NUMBER: US/09/709.126

.....

1

GENERAL INFORMATION:
 APPLICANT: Kraus, Matthias H.
 APPLICANT: Aaronson, Stuart A.
 TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE
 TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THERE TO, AND
 TITLE OF INVENTION: BIOASSAYS AND METHODS RELATED THERE TO
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Suite 400
 STREET: 133 Carnegie Way, N.W.
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.A.
 ZIP: 30303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/473,119
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/978,895
 FILING DATE: 10-NOV-1992
 APPLICATION NUMBER: US 07/444,406
 FILING DATE: 01-DEC-1989
 ATTORNEY/AGENT INFORMATION:

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 08:37:41 ; Search time 97 Seconds
(without alignments)
15.013 Million cell updates/sec

Title: 09-833799-13B
Perfect score: 327
Sequence: 1 aqepvkgpvtkpgscpiil.....cpgikkcecgscgmcfvpq 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	233	71.3	40	10 US-09-757-908A-7	Sequence 7, Appli
2	161	49.2	131	10 US-09-790-264-61	Sequence 61, Appli
3	143	43.7	132	10 US-09-865-812-2	Sequence 2, Appli
4	112	34.3	111	9 US-09-992-598-345	Sequence 345, App
5	112	34.3	111	9 US-09-989-293A-345	Sequence 345, App
6	112	34.3	111	9 US-09-989-735-345	Sequence 345, App
7	112	34.3	111	9 US-09-990-444-345	Sequence 345, App
8	112	34.3	111	9 US-09-989-730-345	Sequence 345, App
9	112	34.3	111	9 US-09-990-436-345	Sequence 345, App
10	112	34.3	111	9 US-09-991-181-345	Sequence 345, App
11	112	34.3	111	9 US-09-993-687-345	Sequence 345, App
12	112	34.3	111	9 US-09-997-653-345	Sequence 345, App
13	112	34.3	111	9 US-09-993-667-345	Sequence 345, App
14	112	34.3	111	9 US-09-990-438-345	Sequence 345, App
15	112	34.3	111	9 US-09-990-562-345	Sequence 345, App
16	112	34.3	111	9 US-09-997-428-345	Sequence 345, App
17	112	34.3	111	9 US-09-997-666-345	Sequence 345, App
18	112	34.3	111	10 US-09-989-722-345	Sequence 345, App
19	112	34.3	111		

20	112	34.3	111	10	US-09-989-723-345	Sequence 345, App
21	112	34.3	111	10	US-09-989-279-345	Sequence 345, App
22	112	34.3	111	10	US-09-989-727-345	Sequence 345, App
23	112	34.3	111	10	US-09-989-731-345	Sequence 345, App
24	112	34.3	111	10	US-09-989-732-345	Sequence 345, App
25	112	34.3	111	10	US-09-991-073-345	Sequence 345, App
26	112	34.3	111	10	US-09-990-442-345	Sequence 345, App
27	112	34.3	111	10	US-09-991-163-345	Sequence 345, App
28	112	34.3	111	10	US-09-993-604-345	Sequence 345, App
29	112	34.3	111	10	US-09-990-456-345	Sequence 345, App
30	112	34.3	111	10	US-09-989-721-345	Sequence 345, App
31	101.5	31.0	60	10	US-09-790-264-59	Sequence 59, Appl
32	96.5	29.5	74	10	US-09-790-264-58	Sequence 58, Appl
33	94.5	28.9	59	10	US-09-790-264-67	Sequence 67, Appl
34	94.5	28.9	72	10	US-09-823-038A-38	Sequence 38, Appl
35	94.5	28.9	76	10	US-09-790-264-56	Sequence 56, Appl
36	93	28.4	124	9	US-09-924-340-42	Sequence 42, Appl
37	93	28.4	124	9	US-09-992-600A-42	Sequence 42, Appl
38	93	28.4	137	10	US-09-925-300-1361	Sequence 1361, Ap
39	92.5	28.3	679	12	US-10-119-714-1	Sequence 1, Appli
40	85	26.0	133	9	US-09-852-797-75	Sequence 75, Appl
41	85	26.0	133	10	US-09-853-161-75	Sequence 75, Appl
42	85	26.0	133	10	US-09-852-659A-75	Sequence 75, Appl
43	80.5	24.6	117	10	US-09-852-659A-119	Sequence 119, App
44	75.5	23.1	102	10	US-09-852-659A-120	Sequence 120, App
45	73.5	22.5	70	10	US-09-894-882-241	Sequence 241, App
46	73.5	22.5	70	10	US-09-894-882-250	Sequence 250, App
47	72	22.0	548	10	US-09-819-136-2	Sequence 2, Appli
48	69	21.1	49	10	US-09-864-761-34921	Sequence 34921, A
49	64.5	19.7	70	10	US-09-894-882-244	Sequence 244, App
50	64.5	19.7	70	10	US-09-894-882-256	Sequence 256, App
51	64.5	19.7	70	10	US-09-894-882-350	Sequence 350, App
52	64	19.6	76	9	US-09-749-637A-333	Sequence 333, App
53	61	18.7	32	10	US-09-894-882-476	Sequence 476, App
54	61	18.7	44	10	US-09-894-882-459	Sequence 459, App
55	61	18.7	44	10	US-09-894-882-462	Sequence 462, App
56	61	18.7	44	10	US-09-894-882-488	Sequence 488, App
57	61	18.7	44	10	US-09-894-882-489	Sequence 489, App
58	60.5	18.5	70	10	US-09-894-882-235	Sequence 235, App
59	60.5	18.5	70	10	US-09-894-882-253	Sequence 253, App
60	60.5	18.5	70	10	US-09-894-882-262	Sequence 262, App
61	59.5	18.2	69	10	US-09-894-882-265	Sequence 265, App
62	59	18.0	32	10	US-09-894-882-477	Sequence 477, App
63	59	18.0	67	10	US-09-894-882-286	Sequence 286, App
64	59	18.0	70	10	US-09-894-882-353	Sequence 353, App
65	59	18.0	173	10	US-09-915-582-97	Sequence 97, Appl
66	58.5	17.9	69	10	US-09-894-882-232	Sequence 232, App
67	58.5	17.9	84	10	US-09-864-761-42841	Sequence 42841, A
68	58	17.7	44	10	US-09-894-882-242	Sequence 242, App
69	58	17.7	44	10	US-09-894-882-251	Sequence 251, App
70	58	17.7	106	12	US-10-012-076-1	Sequence 1, Appli
71	58	17.7	384	10	US-09-815-242-10742	Sequence 10742, A
72	58	17.7	2813	10	US-09-886-900-2	Sequence 2, Appli
73	57.5	17.6	31	10	US-09-894-882-472	Sequence 472, App
74	57.5	17.6	41	10	US-09-894-882-504	Sequence 504, App
75	57.5	17.6	4679	10	US-09-804-898-2	Sequence 2, Appli
76	56.5	17.3	69	10	US-09-894-882-271	Sequence 271, App
77	56.5	17.3	112	9	US-09-738-626-5264	Sequence 5264, Ap
78	56	17.1	32	10	US-09-894-882-478	Sequence 478, App
79	56	17.1	55	10	US-09-864-761-38020	Sequence 38020, A
80	56	17.1	70	10	US-09-894-882-356	Sequence 356, App
81	56	17.1	234	10	US-09-915-593-2	Sequence 2, Appli
82	56	17.1	241	10	US-09-915-593-28	Sequence 28, Appl
83	56	17.1	241	12	US-10-116-378-3	Sequence 3, Appli
84	56	17.1	265	10	US-09-871-388-6	Sequence 6, Appli
85	56	17.1	282	9	US-09-905-291A-127	Sequence 127, App
86	56	17.1	282	9	US-09-902-853-127	Sequence 127, App
87	56	17.1	282	9	US-09-907-824-127	Sequence 127, App
88	56	17.1	282	9	US-09-907-841-127	Sequence 127, App
89	56	17.1	282	9	US-09-904-011-127	Sequence 127, App
90	56	17.1	282	9	US-10-028-072-312	Sequence 312, App
91	56	17.1	282	9	US-09-906-742-127	Sequence 127, App
92	56	17.1	282	9	US-10-121-049-312	Sequence 312, App

93 56 17.1 282 9 US-10-123-904-312 Sequence 312, App
94 56 17.1 282 9 US-10-140-470-312 Sequence 312, App
95 56 17.1 282 9 US-09-906-838-127 Sequence 127, App
96 56 17.1 282 9 US-09-907-613-127 Sequence 127, App
97 56 17.1 282 9 US-09-907-942-127 Sequence 127, App
98 56 17.1 282 9 US-10-175-746-312 Sequence 312, App
99 56 17.1 282 9 US-10-176-918-312 Sequence 312, App
100 56 17.1 282 9 US-10-176-921-312 Sequence 312, App

ALIGNMENTS

RESULT 1
US-09-757-908A-7
; Sequence 7, Application US/09757908A
; Patent No. US20020052468A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; TITLE OF INVENTION: Disulfide Core Polypeptides
; FILE REFERENCE: 98-13D1
; CURRENT APPLICATION NUMBER: US/09/757,908A
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 09/326,039
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: US 60/088,136
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-908A-7

Query Match 71.3%; Score 233; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 9.9e-17;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 IILIRCAMLPPNRLCKDTCPIGKKCEGSCGMACFVPQ 57
Db 1 IILIRCAMLPPNRLCKDTCPIGKKCEGSCGMACFVPQ 40

RESULT 2
US-09-790-264-61
; Sequence 61, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-790-264-61

Query Match 49.2%; Score 161; DB 10; Length 131;
Best Local Similarity 52.8%; Pred. No. 2.8e-09;
Matches 28; Conservative 3; Mismatches 22; Indels 0; Gaps 0;

Qy 4 PVKGPVSTKPGSCPIILIRCAMLPPNRLCKDTCPIGKKCEGSCGMACFVP 56
Db 78 PIRKPVWRKPGRCVKVTQARCMMLNPPNVCQDGGQCDGKYKCCGICGKVCLPP 130

RESULT 3
US-09-865-812-2
; Sequence 2, Application US/09865812
; Patent No. US20020115626A1
; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Method of Detecting inflammatory Lung Disorders
; FILE REFERENCE: 21402-018 US
; CURRENT APPLICATION NUMBER: US/09/865,812
; CURRENT FILING DATE: 2001-05-28
; PRIOR APPLICATION NUMBER: 60/207,104
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-812-2

Query Match 43.7%; Score 143; DB 10; Length 132;
Best Local Similarity 48.2%; Pred. No. 1.6e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

Qy 3 EPVKGPVST--KPGSCPIILIRCAMLPPNRLCKDTCPIGKKCEGSCGMACFVP 56
Db 74 DPVDTNPTRRRKPGKCPVTYGGQCLMLNPPNFCMDGQCKRDLKCCMGKSCVSP 129

RESULT 4
US-09-992-598-345
; Sequence 345, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
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PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090690

; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;

Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AQEPVKGVPSTKPGSCPIILIRCAMLNPPNRLKDTDCBGIKKCCGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVP 73

RESULT 5

US-09-989-293A-345

; Sequence 345, Application US/09989293A

; Patent No. US20020177164A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tunas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C66

; CURRENT APPLICATION NUMBER: US/09/989,293A

; CURRENT FILING DATE: 2001-11-20

; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR FILING DATE: 1998-06-03
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQBPVKGPVSTKPGSCPIILIRCAMLNPPNRCILKDTDCPGIKKCCGSGCMACFVP 56

Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGRKCVIP 73

RESULT 6

US-09-989-735-345

; Sequence 345, Application US/09989735

; Publication No. US20020193299A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR APPLICATION NUMBER: 60/091633
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match      34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;
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Db      20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73
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RESULT 7

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US-09-990-444-345
; Sequence 345, Application US/09990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/088876
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      34.3%; Score
Best Local Similarity 42.9%; Pred
Matches 24; Conservative 6; M

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Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDP

RESULT 8
US-09-989-730-345
; Sequence 345, Application US/09989973
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Tr
; FILE REFERENCE: P2730P1C69
; CURRENT APPLICATION NUMBER: US/09/9
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/087607

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2

PRIOR APPLICATION NUMBER: 60/089900	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349	PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355	PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542	PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090696	PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862	PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863	PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360	PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478	PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544	PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519	PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091982	PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182	PRIOR FILING DATE: 1998-07-07

; PRIOR FILING DATE: 1998-07-09
Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;
QY 1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCKFSDPP-QCHTDQDCLGERKCCYLHCCKFCVIP 73

RESULT 9

US-09-990-436-345
; Sequence 345, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C14
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Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AQEPVKGPVSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVP 73

RESULT 11
US-09-993-687-345
; Sequence 345, Application US/09993687

; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 34.3%; Score 112; DB 9; Length 111;
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Qy 1 AQEPVKGVPSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73

RESULT 12

US-09-989-734-345
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; Publication No. US20030003531A1
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Oy 1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTPGIIKKCEGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCKSDPP-QCHTDQDCLGERKCCYLHCGFKCVP 73

RESULT 13
US-09-997-653-345
; Sequence 345, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;

Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRLKXDTDCPGIKKCCGSGCMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73

RESULT 14

US-09-993-667-345
; Sequence 345, Application US/09993667
; Publication No. US20030022187A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC4
; CURRENT APPLICATION NUMBER: US/09/993,667
; CURRENT FILING DATE: 2001-11-14
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;
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;
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; PRIOR APPLICATION NUMBER: 60/092182
;
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;

Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGCGMACFVP 56

Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGPKCVIP 73

RESULT 15

US-09-990-438-345
; Sequence 345, Application US/09990438
; Publication No. US20030027754A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

;	PRIOR APPLICATION NUMBER: 60/088876
;	PRIOR FILING DATE: 1998-06-11
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;

Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQBPVKGPVSTKPGSCPIILIRCAMLPPNRLKDTDCPGIKKCEGSCGMACFVP 56

Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDDCLGERKCCYLHCGFKCVIP 73

RESULT 16

US-09-990-562-345

; Sequence 345, Application US/09990562

; Publication No. US20030027985A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C18
; CURRENT APPLICATION NUMBER: US/09/990,562
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186
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[illegible]

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; PRIOR APPLICATION NUMBER: 60/091988
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Scor
Best Local Similarity 42.9%; Pred
Matches 24; Conservative 6; M

QY 1 AQEPVKPVSVKPGSCPIILIRCAMLNP
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDP

RESULT 19
US-09-989-722-345
; Sequence 345, Application US/0998972
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secretd and Tr
; TITLE OF INVENTION: Acids Encoding
; FILE REFERENCE: P2730PlC63
; CURRENT APPLICATION NUMBER: US/09/99
; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/087759

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; Patent No. US20020072092A1										
; GENERAL INFORMATION:										
; APPLICANT: Ashkenazi, Avi J.										
; APPLICANT: Baker, Kevin P.										
; APPLICANT: Botstein, David										
; APPLICANT: Desnoyers, Luc										
; APPLICANT: Eaton, Dan L.										
; APPLICANT: Ferrara, Napoleone										
; APPLICANT: Fong, Sherman										
; APPLICANT: Gerber, Hanspeter										
; APPLICANT: Gerritsen, Mary E.										
; APPLICANT: Goddard, Audrey										
; APPLICANT: Godowski, Paul J.										
; APPLICANT: Grimaldi, J.Christopher										
; APPLICANT: Gurney, Austin L.										
; APPLICANT: Kljavin, Ivar J.										
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; APPLICANT: Stewart, Timothy A.										
; APPLICANT: Tumas, Daniel										
; APPLICANT: Watanabe, Colin K.										
; APPLICANT: Williams, P. Mickey										
; APPLICANT: Wood, William I.										
; APPLICANT: Zhang, Zemin										
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic										
; TITLE OF INVENTION: Acids Encoding the Same										
; FILE REFERENCE: P2730P1C62										
; CURRENT APPLICATION NUMBER: US/09/989,723										
; PRIOR FILING DATE: 2001-11-19										
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
DB 20 AVEGVKEGIE-KAGVCPADNVRCKFSKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73

RESULT 21
US-09-989-279-345
; Sequence 345, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/091982	PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182	PRIOR FILING DATE: 1998-07-09

Matches	24;	Conservative	6;	Mismatches	24;	Indels	2;	Gaps	2;
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RESULT 22

US-09-989-727-345
; Sequence 345, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 34.3%; Score 112; DB 10; Length 111;

Best Local Similarity 42.9%; Pred. No. 0.00014;

Sequence similarity	100%	90%	80%	70%	60%	50%	40%	30%	20%	10%	0%
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RESULT 23

US-09-989-731-345

; Sequence 345, Application US/09989731

Patent No. US20020103125A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PlC70
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AQEPVKGPVSTKPGSCPILIRCAMLNPPNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73

RESULT 24
US-09-989-732-345
; Sequence 345, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQBVPKPVSTKPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFPV 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73

RESULT 25

US-09-991-073-345
; Sequence 345, Application US/09991073
; Patent No. US20020127576A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 34.3%; Score 112; DB 10; Length 111;
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Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

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Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73

RESULT 26

US-09-990-442-345
; Sequence 345, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
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Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQBPVKGPVSTKPGSCPILIRCAMLNPPNRCLKDTDCPGIKKCCGSGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDDCLGERKCCYLHCGRKCVIP 73

RESULT 28

US-09-993-604-345
; Sequence 345, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322

;	PRIOR APPLICATION NUMBER:	60/089600
;	PRIOR FILING DATE:	1998-06-17
;	PRIOR APPLICATION NUMBER:	60/089653
;	PRIOR FILING DATE:	1998-06-17
;	PRIOR APPLICATION NUMBER:	60/089801
;	PRIOR FILING DATE:	1998-06-18
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;	PRIOR FILING DATE:	1998-06-18
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQEPVKGPVSTKPGSCPILIRCAMLNPPNRCCLKDTCPGIKKCCGSGCMACFVP 56
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Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73

RESULT 29
US-09-990-456-345
; Sequence 345, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;
QY 1 AQEPVKGPVSTKPGSCPILIRCAMLNPPNRCUKDTCDCPGIKKCCGSGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73

RESULT 30

US-09-989-721-345
; Sequence 345, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P27301C55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021

100


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; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compositions Isolated From Stromal Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1037c3
; CURRENT APPLICATION NUMBER: US/09/823,038A
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Mouse
US-09-823-038A-38
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Query Match 28.9%; Score 94.5; DB 10; Length 72;
Best Local Similarity 35.8%; Pred. No. 0.0047;
Matches 19; Conservative 3; Mismatches 14; Indels 17; Gaps 2;

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QY 12 KPGSCPILLIRCAMLNPP-----NRCLKDTCPCGIKKCCGSCGMACFVP 56
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Db 27 KPGACP-----KPSPEVGVICVDQCSDGSGCPGNMKCCSNCSGHVCKTP 70
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RESULT 35

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US-09-790-264-56
; Sequence 56, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
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; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
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; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(17)
US-09-790-264-56
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Query Match 28.9%; Score 94.5; DB 10; Length 76;
Best Local Similarity 35.8%; Pred. No. 0.0049;
Matches 19; Conservative 3; Mismatches 14; Indels 17; Gaps 2;

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QY 12 KPGSCPILLIRCAMLNPP-----NRCLKDTCPCGIKKCCGSCGMACFVP 56
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Db 31 KPGACP-----KPSPEVGVICVDQCSDGSGCPGNMKCCSNCSGHVCKTP 74
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RESULT 36
US-09-924-340-42
; Sequence 42, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 42
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..30
US-09-924-340-42
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Query Match 28.4%; Score 93; DB 9; Length 124;
Best Local Similarity 40.4%; Pred. No. 0.011;
Matches 19; Conservative 6; Mismatches 20; Indels 2; Gaps 2;

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QY 12 KPGSCPILLIRCAMLN-PPNRCLKDTCPCGIKKCCGSCG-MACFVP 56
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Db 76 KEGSCPQVNFQPLGLCRDQCQVDSQCPGQMKCCRNCGKVCVTP 122
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RESULT 37

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US-09-992-600A-42
; Sequence 42, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
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; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 42
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..30
US-09-992-600A-42
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Query Match 28.4%; Score 93; DB 9; Length 124;
Best Local Similarity 40.4%; Pred. No. 0.011;
Matches 19; Conservative 6; Mismatches 20; Indels

12 KPGSCPIILIRCAMLN-ppNRCLKDTDCPGIKKCEGSCG-MACFVP 56

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RESULT 38
US-09-925-300-1361
; Sequence 1361, Application US/09925300
; Patent No. US20020151681A1

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; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
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US-09-925-300-1361

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Query Match 28.4%; Score 93; DB 10; Length 137;
Best Local Similarity 40.4%; Pred. No. 0.012;
Matches 19; Conservative 6; Mismatches 20; Indels

Qy 12 KPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCEGSCG-MACFVP 56
Db 89 KEGSCPOVINFPOLGLCRDQCQVDSQCPGOMKCCRNCGKGVSCVTP 135

RESULT 39
US-10-119-714-1
; Sequence 1, Application US/10119714
; Patent No. US20020123467A1

```

; APPLICANT: PETIT, CHRISTINE
; APPLICANT: SOUSSI-YANICOSTAS, NADIA
; APPLICANT: HARDELIN, JEAN-PIERRE
; APPLICANT: SARAILH, CATHERINE
; APPLICANT: ROUGON, GENEVIEVE
; APPLICANT: LEGOUIS, RENAUD
; APPLICANT: ARDOUIN, OLIVIER
; APPLICANT: MAZIE, JEAN-CLAUDE
; TITLE OF INVENTION: THERAPEUTIC COMPOSITION COMPRISING KAL PROTEIN AND USE
; TITLE OF INVENTION: OF THE KAL PROTEIN FOR THE TREATMENT OF RETINAL, RENAL,
; TITLE OF INVENTION: NEURONAL AND NEURAL INJURY
; FILE REFERENCE: 0660-0151-0XPCT
; CURRENT APPLICATION NUMBER: US/10/119,714
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/319,236
; PRIOR FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-119-714-1

```

Query Match	28.3%	Score 92.5;	DB 12;	Length 679;
Best Local Similarity	34.6%	Pred. No. 0.056;		
Matches 18; Conservative	3;	Mismatches 20;	Indels 11	

Qy 12 KPGSCPI-----ILIRCAMLPPNRLKDTDCPIGIKKCEGSCGMACFVPQ 57
 Db 130 KQGDCPAPEKASGFAAACV-----ESCEVDNECSGVKKCCSNGCGHTCQVPK 176

RESULT 40
US-09-852-797-75
; Sequence 75, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-75

Query Match	26.0%;	Score 85;	DB 9;	Length 133;
Best Local Similarity	40.4%;	Pred. No. 0.068;		
Matches 21;	Conservative	2;	Mismatches 25;	Indels 4;
				Gaps 2;

[illegible]

```

RESULT 41
US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12

```

```

RESULT 42
US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 75
; LENGTH: 133

```

RESULT 44
US-09-852-659A-120
; Sequence 120, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852-659A

```
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120
```

```
Query Match      23.1%; Score 75.5; DB 10; Length 102;
Best Local Similarity 42.1%; Pred. No. 0.45;
Matches 16; Conservative 1; Mismatches 20; Indels 1; Gaps 1;
```

```
QY 16 CPILIRCA-MLNPPNRLKDTDCPGIKKCCGSCGMAC 53
||| | | | | | | | | | | | | | | | | | | | |
Db 2 CPKIRECE-FQERDVCTKDRQCQDNKKCCVFCGKKC 38
```

```
RESULT 45
US-09-894-882-241
; Sequence 241, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
```

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; SEQ ID NO 241
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-241
```

```
Query Match      22.5%; Score 73.5; DB 10; Length 70;
Best Local Similarity 37.5%; Pred. No. 0.5;
Matches 18; Conservative 8; Mismatches 15; Indels 7; Gaps 3;
```

```
QY 15 SCPIILIRCA-MLNPPNRLKDTDCPGI-----KKCCGSCGMACFV 55
||| | | | | | | | | | | | | | | | | | | | |
Db 9 SCFLLVIVCLNLVILINACYQDETPCRGSTFCRRKKCCIGTCRFPYV 56
```

```
RESULT 46
US-09-894-882-250
; Sequence 250, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-250
```

```
Query Match      22.5%; Score 73.5; DB 10; Length 70;
Best Local Similarity 37.5%; Pred. No. 0.5;
Matches 18; Conservative 8; Mismatches 15; Indels 7; Gaps 3;
```

```
QY 15 SCPIILIRCA-MLNPPNRLKDTDCPGI-----KKCCGSCGMACFV 55
||| | | | | | | | | | | | | | | | | | | | |
Db 9 SCFLLVIVCLNLVILINACYQDETPCRGSTFCRRKKCCIGTCRFPYV 56
```

```
RESULT 47
US-09-819-136-2
; Sequence 2, Application US/09819136
; Patent No. US20020146789A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR
; FILE REFERENCE: 00-25
; CURRENT APPLICATION NUMBER: US/09/819,136
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/193,642
```


RESULT 53
US-09-894-882-476
; Sequence 476, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238

Db 1 CYQDETPCRGSI FCCRKKCCIGTCRFFPCYV 30

APPLICANT: University of Utah Research Foundation


```
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-253

Query Match      18.5%; Score 60.5; DB 10; Length 70;
Best Local Similarity 30.6%; Pred. No. 9.1;
Matches 15; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 15 SCPIILIRCA-MLNPPNRCLKD-----TDCPGIKKCCGSCGCMACFV 55
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 9 SCFLLVIACLNLVLTNACLRLDGQSCGYHSDCCRY-SCCWGYCDQKCLI 56

RESULT 60
US-09-894-882-262
; Sequence 262, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 262
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-262

Query Match      18.5%; Score 60.5; DB 10; Length 70;
Best Local Similarity 30.6%; Pred. No. 9.1;
Matches 15; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 15 SCPIILIRCA-MLNPPNRCLKD-----TDCPGIKKCCGSCGCMACFV 55
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 9 SCFLLVIACLNLVLTNACLRLDGQSCGYHSDCCRY-SCCWGYCDQKCLI 56

RESULT 61
US-09-894-882-265
; Sequence 265, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
```

```
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 265
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-265

Query Match      18.2%; Score 59.5; DB 10; Length 69;
Best Local Similarity 35.7%; Pred. No. 11;
Matches 15; Conservative 8; Mismatches 14; Indels 5; Gaps 3;

QY 15 SCPIILIRCA-MLNPPNRCLKDT-DCPGIKKCCGSCGCMACF 54
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 9 SCFLLVIVCLNLVLTNACLHETPPCRRSFQCCHGNC---CF 47

RESULT 62
US-09-894-882-477
; Sequence 477, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 477
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus episcopatatus
US-09-894-882-477

Query Match      18.0%; Score 59; DB 10; Length 32;
Best Local Similarity 38.2%; Pred. No. 6.3;
Matches 13; Conservative 1; Mismatches 18; Indels 2; Gaps 1;
```

100

100

100

Query Match 17.7%; Score 58; DB 10; Length 384;
Best Local Similarity 44.8%; Pred. NO. 74;
Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 30 NRCLKDTPGKCCG--SCGMACFVP 56
| : | | | | | : | | | | : |
Db 67 NHDVMDNDAGIKVMSEGLLSGVTSLP 95

RESULT 72

US-09-886-900-2
; Sequence 2, Application US/09886900
; Patent No. US20020137051A1
; GENERAL INFORMATION:
; APPLICANT: Venta, Patrick J
; Yuzbasiyan-Gurkan, Vilma
; Schall, William D
; Brewer, George J
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND
; FACTOR AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: 5445 Corporate Drive
; CITY: Troy
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48098

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/886,900
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/896,449
; FILING DATE: 18-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REFERENCE/DOCKET NUMBER: 2115-001226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 248-641-1600
; TELEFAX: 248-641-0270
; TELEX: 287637

INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2813 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-886-900-2

Query Match 17.7%; Score 58; DB 10; Length 2813;
Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 2; Mismatches 9; Indels 16; Gaps 5;

QY 23 CAMLNPP----NRCLKDTPGKCCG---SCG----MACFVP 56
| | | | | : | | : | | | | |
Db 2199 CAMSCPPLVYNHC--EHGCP---RLCEGNTSSCGDQPSGCFCP 2238

RESULT 73

US-09-894-882-472
; Sequence 472, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.

; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 472
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus figulinus
US-09-894-882-472

Query Match 17.6%; Score 57.5; DB 10; Length 31;
Best Local Similarity 42.3%; Pred. No. 8.6;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 31 RCLKDTPGKCCGSCGMACFVP 56
| | | : | : | | | | : |
Db 7 RCEPDSQCE-SECCMGSCANPCRP 31

RESULT 74

US-09-894-882-504
; Sequence 504, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 504
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Conus figulinus

Search completed: February 11, 2003, 08:46:46
Job time : 99 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 08:35:56 ; Search time 36 Seconds
(without alignments)
210.980 Million cell updates/sec

Title: 09-833799-13B
Perfect score: 327
Sequence: 1 aqepvkgpvstkggscpiil.....cpgikkcccgsgmacfvpq 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq 101002:*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	327	100.0	57	11	AA08217 Human leukocyte el
2	324	99.1	57	15	AA048552 Elafin derivative
3	324	99.1	142	19	AA07237 pPIC9/ELF25L cDNA
4	323	98.8	57	15	AA048553 Elafin derivative
5	323	98.8	57	15	AA048554 Elafin derivative
6	321	98.2	57	19	AA057223 Elafin. Synthetic
7	233	71.3	40	21	AA049447 Porcine elafin FLE
8	233	71.3	40	22	AA04337 Human FLE peptide.
9	233	71.3	40	23	AA023762 Porcine elafin (FL
10	179.5	54.9	166	15	AA050335 SPAI pre-sequence

11	179.5	54.9	189	15	AA050334 SPAI peptide. Sus
12	177.5	54.3	61	11	AA08145 Generic sodium pot
13	174.5	53.4	61	11	AA08146 Sodium potassium A
14	172	52.6	49	22	AA092379 Miscellaneous pept
15	161	49.2	126	20	AA098909 Mouse IMC carcinom
16	161	49.2	131	20	AA098908 Mouse IMC carcinom
17	147	45.0	60	15	AA051175 CLPI analogue (Gly
18	147	45.0	60	15	AA051176 CLPI analogue (Val
19	146	44.6	60	15	AA051172 CLPI. Homo sapien
20	145	44.3	60	15	AA051174 CLPI analogue (Phe
21	143	43.7	58	18	AA01843 Antileukoprotease
22	143	43.7	58	18	AA01844 Antileukoprotease
23	143	43.7	60	21	AA053100 Serine protease in
24	143	43.7	60	21	AA079951 Truncated SLPI pro
25	143	43.7	60	22	AA065997 Secretory leukocyt
26	143	43.7	90	8	AA070583 Sequence of protei
27	143	43.7	91	21	AA053102 Serine protease in
28	143	43.7	106	9	AA082403 Synthetic protein
29	143	43.7	107	7	AA060562 Synthetic sequence
30	143	43.7	107	7	AA060563 Serine protease in
31	143	43.7	107	9	AA082597 Synthetic sequence
32	143	43.7	107	10	AA090384 Human polymorphon
33	143	43.7	107	20	AA017426 Human serine prote
34	143	43.7	107	21	AA053101 Serine protease in
35	143	43.7	107	22	AA065993 Recombinant serine
36	143	43.7	107	22	AA047402 SLPI native mature
37	143	43.7	107	23	AA099874 Human secretory le
38	143	43.7	107	23	AA075058 Human seine protea
39	143	43.7	107	23	AA075061 Human serine prote
40	143	43.7	108	21	AA053105 Serine protease in
41	143	43.7	132	8	AA070584 Sequence of protei
42	143	43.7	132	17	AA084056 Secretory leukocyt
43	143	43.7	132	22	AB050282 Leukocyte protease
44	143	43.7	132	22	AA047403 SLPI native immatu
45	143	43.7	132	22	AA066864 Human antileukopro
46	143	43.7	132	23	AA011763 Human antileukopro
47	143	43.7	503	23	AA099881 SLAP1 fusion prote
48	143	43.7	503	23	AA099884 rSLAP1 fusion prot
49	142	43.4	107	20	AA094482 Serine protease in
50	141	43.1	53	10	AA090126 Human polymorphon
51	141	43.1	53	13	AA020553 SLPI C-terminal.
52	141	43.1	53	13	AA022029 Elastase inhibitor
53	141	43.1	53	14	AA030482 Blood coagulation
54	141	43.1	53	18	AA01847 Antileukoprotease
55	141	43.1	53	18	AA01850 Antileukoprotease
56	141	43.1	57	21	AA053103 Serine protease in
57	141	43.1	58	18	AA01851 Antileukoprotease
58	140	42.8	58	18	AA01845 Antileukoprotease
59	140	42.8	58	18	AA01846 Antileukoprotease
60	140	42.8	107	22	AA047404 SLPI oxidation-res
61	140	42.8	132	22	AA047405 SLPI oxidation-res
62	139.5	42.7	101	21	AA053106 Human SLPI peptide
63	139.5	42.7	101	22	AA065996 Recombinant secret
64	139	42.5	98	17	AA000663 Mutein #1 of secre
65	139	42.5	98	17	AA000664 Mutein #2 of secre
66	139	42.5	98	17	AA000665 Mutein #3 of secre
67	139	42.5	98	17	AA000666 Mutein #4 of secre
68	139	42.5	98	17	AA000662 Residues 5-102 of
69	138	42.2	107	20	AA017425 Human serine prote
70	136	41.6	49	7	AA060566 Synthetic sequence
71	136	41.6	49	15	AA050084 Elastase-inhibiti
72	136	41.6	49	15	AA058594 Secretory leukocyt
73	136	41.6	49	16	AA075184 Secretory leukocyt
74	136	41.6	49	16	AA066284 Polypeptide fragme
75	136	41.6	49	18	AA01848 Antileukoprotease
76	136	41.6	49	21	AA053104 Serine protease in
77	136	41.6	50	15	AA050083 Elastase-inhibiti
78	136	41.6	50	15	AA058595 Secretory leukocyt
79	136	41.6	50	16	AA075185 Secretory leukocyt
80	136	41.6	50	16	AA066285 Polypeptide fragme
81	136	41.6	50	21	AA069878 Secretory Leukocyt
82	136	41.6	51	17	AA000653 Residues 57-107 of
83	136	41.6	51	17	AA000656 Mutein #1 of secre

XX Elafin; elafin 25L gene; Pichia pastoris; expression vector;
KW alcohol oxidase 1; controlling region; promoter.
XX
OS Synthetic.
OS Pichia pastoris.

XX Key Location/Qualifiers
FH Peptide 1..85
FT /label= signal
FT Protein 86..142
FT /label= elafin_25L
XX

PN JPI0127292-A.

XX 19-MAY-1998.

PF 31-OCT-1996; 96JP-0304233.

PR 31-OCT-1996; 96JP-0304233.

XX (TSUR) TSUMURA & CO.

XX WPI; 1998-340667/30.

DR N-PSDB; AAV28852.

XX New elafin expression vector - used to transform microbial host(s)
PT for production of elafin commercially

PS Example 1; Page 11-15; 21pp; Japanese.

XX The present sequence represents the protein from the pPIC9/ELF25L cDNA
CC construct containing the elafin 25L gene, used in an example of the
CC present invention. The present invention describes: (1) an elafin (EL)
CC expression vector comprising a gene encoding EL and a gene encoding
CC alcohol oxidase 1 controlling region (AOCR) which controls the
CC expression of EL encoding gene; (2) a microbial host transformed with
CC the vector; (3) DNA fragment for recombinant transformation comprising:
CC (a) a first region homologous to the genomic DNA of the host; (b) a
CC promoter region of (AOCR) gene; (c) a gene encoding signal peptide; (d)
CC a linker designed to secrete a matured elafin; (e) a gene encoding EL;
CC (f) selection marker gene; (g) stop codon, and (h) a second region
CC homologous to a part of the genomic DNA of the host, and (4) a microbial
CC host transformed with the DNA fragment of (3). The microbial hosts can
CC be used to prepare EL commercially. The production of EL by the
CC microbial hosts can be carried on a large scale.

XX Sequence 142 AA;

Query Match 99.1%; Score 324; DB 19; Length 142;
Best Local Similarity 98.2%; Pred. No. 1.7e-26;
Matches 56; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQEPVKGPVSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57
Db 86 AQEPVKGPVSTKPGSCPILIRCALLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 142

RESULT 4

AAR48553
ID AAR48553 standard; Protein; 57 AA.

XX AAR48553;

XX 23-SEP-1994 (first entry)

DE Elafin derivative Val25.

XX Elafin; derivative; mutation; transformation; E. coli; yeast;
KW Bacillus subtilis; elastase inhibitor; oxidation.

XX Synthetic.

PN WO9404697-A.
XX
PD 03-MAR-1994.
XX
PF 11-AUG-1993; 93WO-JP01133.
XX
PR 11-AUG-1992; 92JP-0234085.
XX
PA (TSUR) TSUMURA & CO.
XX
PI Amagaya S, Ishima Y, Kaji A, Okawa N, Yoshida M;
XX WPI; 1994-083211/10.
DR N-PSDB; AAQ56675.
XX
PT Recombinant modified elafin with improved oxidation stability -
XX has pharmaceutical use as an elastase inhibitor
PS Claim 1; Page 24; 35pp; Japanese.

XX The sequences given in AAR48552-54 represent elafin derivatives. The
CC DNA encoding wild type elafin is mutated, inserted into a suitable
CC vector and then used to transform E. coli, yeast, Bacillus subtilis
CC or animal cells. The modified elafin is expressed when the
CC transformed cells are cultured. The modified elafin are drugs with
CC elastase inhibitor activity. They have improved oxidation stability
CC over natural elafin and thus retain activity better under oxidative
CC conditions.

XX Sequence 57 AA;

Query Match 98.8%; Score 323; DB 15; Length 57;
Best Local Similarity 98.2%; Pred. No. 9e-27;
Matches 56; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQEPVKGPVSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57
Db 1 AQEPVKGPVSTKPGSCPILIRCAVLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57

RESULT 5

AAR48554
ID AAR48554 standard; Protein; 57 AA.

XX AAR48554;

XX 23-SEP-1994 (first entry)

DE Elafin derivative Ile25.

XX Elafin; derivative; mutation; transformation; E. coli; yeast;
KW Bacillus subtilis; elastase inhibitor; oxidation.

XX Synthetic.

PN WO9404697-A.

XX 03-MAR-1994.

PF 11-AUG-1993; 93WO-JP01133.

PR 11-AUG-1992; 92JP-0234085.

XX (TSUR) TSUMURA & CO.

XX Amagaya S, Ishima Y, Kaji A, Okawa N, Yoshida M;

XX WPI; 1994-083211/10.

DR N-PSDB; AAQ56676.

XX Recombinant modified elafin with improved oxidation stability -
PT has pharmaceutical use as an elastase inhibitor
XX

PS Claim 1; Page 25; 35pp; Japanese.

XX The sequences given in AAR48552-54 represent elafin derivatives. The

CC DNA encoding wild type elafin is mutated, inserted into a suitable

CC vector and then used to transform E. coli, yeast, Bacillus subtilis

CC or animal cells. The modified elafin is expressed when the

CC transformed cells are cultured. The modified elafin are drugs with

CC elastase inhibitor activity. They have improved oxidation stability

CC over natural elafin and thus retain activity better under oxidative

CC conditions.

XX

SQ Sequence 57 AA;

Query Match 98.8%; Score 323; DB 15; Length 57;

Best Local Similarity 98.2%; Pred. No. 9e-27;

Matches 56; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQEPVKGPVSTKPGSCPIILIRCAMLPPNPNRCLKDTDCPGIKKCCGSCGMACFVPQ 57

Db 1 AQEPVKGPVSTKPGSCPIILIRCAILNPPNPNRCLKDTDCPGIKKCCGSCGMACFVPQ 57

RESULT 6

AAW57223

ID AAW57223 standard; Protein; 57 AA.

XX

AC AAW57223;

XX

DT 04-AUG-1998 (first entry)

XX

DE Elafin.

XX

KW Elafin; elafin 25L gene; Pichia pastoris; expression vector;

XW alcohol oxidase 1; controlling region; promoter.

XX

OS Synthetic.

OS Pichia pastoris.

XX

FH Key Location/Qualifiers

FT Misc-difference 25 /label= Leu, Ile, Val

FT

XX JP10127292-A.

XX

PD 19-MAY-1998.

XX

PF 31-OCT-1996; 96JP-0304233.

XX

PR 31-OCT-1996; 96JP-0304233.

XX

PA (TSUR) TSUMURA & CO.

XX

DR WPI; 1998-340667/30.

XX

PT New elafin expression vector - used to transform microbial host(s)

PT for production of elafin commercially

XX

PS Claim 4; Page 11; 21pp; Japanese.

XX

CC The present sequence represents elafin from the present invention. The

CC present invention describes: (1) an elafin (EL) expression vector

CC comprising a gene encoding EL and a gene encoding alcohol oxidase 1

CC controlling region (AOCR) which controls the expression of EL encoding

CC gene; (2) a microbial host transformed with the vector; (3) DNA fragment

CC for recombinant transformation comprising: (a) a first region homologous

CC to the genomic DNA of the host; (b) a promoter region of (AOCR) gene; (c)

CC a gene encoding signal peptide; (d) a linker designed to secrete a

CC matured elafin; (e) a gene encoding EL; (f) selection marker gene; (g)

CC stop codon, and (h) a second region homologous to a part of the genomic

CC DNA of the host, and (4) a microbial host transformed with the DNA

CC fragment of (3). The microbial hosts can be used to prepare EL

CC commercially. The production of EL by the microbial hosts can be carried

CC on a large scale.

XX SQ Sequence 57 AA;

Query Match 98.2%; Score 321; DB 19; Length 57;

Best Local Similarity 98.2%; Pred. No. 1.5e-26;

Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AQEPVKGPVSTKPGSCPIILIRCAMLPPNPNRCLKDTDCPGIKKCCGSCGMACFVPQ 57

Db 1 AQEPVKGPVSTKPGSCPIILIRCAIXLPPNPNRCLKDTDCPGIKKCCGSCGMACFVPQ 57

RESULT 7

AAAY49447

ID AAAY49447 standard; peptide; 40 AA.

XX

AC AAAY49447;

XX

DT 17-MAR-2000 (first entry)

XX

DE Porcine elafin FLE polypeptide fragment.

XX

KW Proteinase inhibitor; disulfide core proteinase inhibitor; Zdsc1; mouse;

KW pancreatitis; shock syndrome; hyperfibrinolytic hemorrhage; gene therapy;

XW myocardial infarction; antiinflammatory; vasotropic; cardiant; elafin;

KW FLE.

XX

OS Sus sp.

XX

PN WO9963091-A1.

XX

PD 09-DEC-1999.

XX

PF 04-JUN-1999; 99WO-US12545.

XX

PR 04-JUN-1998; 98US-0090895.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Conklin DC;

XX

DR WPI; 2000-072884/06.

XX

PT Novel polypeptide sequences used as proteinase inhibitors -

XX

PS Disclosure; Page 17; 85pp; English.

XX

CC The invention relates to a new class of proteinase inhibitors called

CC disulfide core proteinase inhibitors (Zdsc1) and provides murine and

CC human Zdsc1 polypeptides. The disulfide core proteins are proteinase

CC inhibitors used for the treatment of acute pancreatitis, various stages

CC of shock syndrome, hyperfibrinolytic hemorrhage and myocardial

CC infarction. Antagonists of the polypeptides can be used as research

CC reagents for characterizing sites of ligand-receptor interaction.

CC Antibodies against the proteins may be used for tagging cells that

CC express the protein, for detecting the protein, and for screening

CC expression libraries. Polynucleotides encoding the polypeptides can be

CC used in gene therapy applications where it is desired to increase or

CC inhibit the protein activity. The present sequence represents a porcine

CC elafin, FLE used in homology studies with Zdsc1 polypeptides.

XX

SQ Sequence 40 AA;

Query Match 71.3%; Score 233; DB 21; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.6e-17;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 IILIRCAMLPPNPNRCLKDTDCPGIKKCCGSCGMACFVPQ 57

Db 1 IILIRCAMLPPNPNRCLKDTDCPGIKKCCGSCGMACFVPQ 40

RESULT 8

AAE04337
ID AAE04337 standard; peptide; 40 AA.
XX
AC AAE04337;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human FLE peptide.
XX
KW Human; antiinflammatory; vasotropic; cardiant; haemostatic; Zdscl;
KW disulphide core protein; serine proteinase inhibitor; acute pancreatitis;
KW shock syndrome; hyperfibrinolytic haemorrhage; myocardial infarction.
XX
OS Homo sapiens.
XX
PN US6239254-B1.
XX
PD 29-MAY-2001.
XX
PF 04-JUN-1999; 99US-0326039.
XX
PR 04-JUN-1998; 98US-0088136.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Conklin DC;
XX
DR WPI; 2001-416774/44.
XX
PT New isolated polypeptides are serine proteinase inhibitors useful for
PT treatment of acute pancreatitis, various states of shock syndrome,
PT hyperfibrinolytic haemorrhage and myocardial infarction.
XX
PS Disclosure; Column 9-10; 24pp; English.
XX
CC The present sequence is human FLE peptide used in the invention. The
CC present invention relates to disulphide core serine proteinase inhibitor
CC Zdscl protein. Zdscl is a member of a new related subfamily referred to
CC as three-disulphide core family. Serine proteinase inhibitors useful for
CC treatment of acute pancreatitis, various states of shock syndrome,
CC hyperfibrinolytic haemorrhage and myocardial infarction.
XX
SQ Sequence 40 AA;

Query Match 71.3%; Score 233; DB 22; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 IILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVPQ 57
Db 1 IILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVPQ 40

RESULT 9
AAE23762
ID AAE23762 standard; Protein; 40 AA.
XX
AC AAE23762;
XX
DT 10-SEP-2002 (first entry)
XX
DE Porcine elafin (FLE) protein.
XX
KW Porcine; disulfide core protein; Zdscl; myocardial infarction; cancer;
KW acute pancreatitis; shock syndrome; transgenic; transgenic animal;
KW hyperfibrinolytic haemorrhage; antisense; gene therapy; vasotropic;
KW antiinflammatory; haemostatic; cardiant; cytosstatic; elafin protein; FLE.
XX
OS Sus sp.
XX
PN US2002052468-A1.
XX
PD 02-MAY-2002.

XX
PF 10-JAN-2001; 2001US-0757908.
XX
PR 04-JUN-1998; 98US-088136P.
PR 04-JUN-1999; 99US-0326039.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Conklin DC;
XX
DR WPI; 2002-415219/44.
XX
PT New isolated disulfide core protein polypeptide for treating acute
PT pancreatitis, various states of shock syndrome, hyperfibrinolytic
PT hemorrhage, myocardial infarction, and cancer -
XX
PS Disclosure; Page 5; 28pp; English.
XX
CC The present invention relates to novel disulfide core protein (Zdscl)
CC proteins and polynucleotides encoding such proteins. Zdscl sequences
CC are serine proteinase inhibitors. They are used to treat myocardial
CC infarction, acute pancreatitis, various states of shock syndrome,
CC hyperfibrinolytic haemorrhage and cancer. Zdscl sequences and their
CC antibodies can be directly or indirectly conjugated to drugs, toxins
CC and radionuclides and used for in vivo diagnostic or therapeutic
CC applications. Fusion proteins containing Zdscl or their antibodies
CC can be used to target cell or tissue inhibition or ablation, e.g.,
CC to treat cancer cells or tissues. Sequences of the invention can be
CC used to produce transgenic or knockout mice. They are also used in
CC gene therapy and antisense gene therapy. The present sequence is
CC porcine elafin protein used in the invention.
XX
SQ Sequence 40 AA;

Query Match 71.3%; Score 233; DB 23; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 IILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVPQ 57
Db 1 IILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVPQ 40

RESULT 10
AAR50335
ID AAR50335 standard; Protein; 166 AA.
XX
AC AAR50335;
XX
DT 17-OCT-1994 (first entry)
XX
DE SPAI pre-sequence peptide.
XX
KW SPAI; sodium ion, potassium ion, ATP-ase inhibitor peptide; cardiac;
KW vascular disease; PCR; polymerase chain reaction.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "pyroglutamyl peptidase"
FT
XX
PN JP06049098-A.
XX
PD 22-FEB-1994.
XX
PF 29-JUL-1992; 92JP-0202286.
XX
PR 29-JUL-1992; 92JP-0202286.
XX
PA (EISA) EISAI CO LTD.
XX
DR WPI; 1994-097819/12.

DR P-PSDB; AAR50334.

XX Sodium ion, potassium ion ATP-ase inhibitor peptide and corresp.

PT DNA - useful to treat cardiac and vascular disease

XX

PS Disclosure; Fig 2; 8pp; Japanese.

XX

CC The sequence (AAQ44862) encodes the SPAI peptide which is useful

CC as a drug for treating cardiac and vascular diseases. The peptide

CC is found as a pre-sequence (AAR50335) which is amplified using

CC primers (AAQ44863-67)

XX

SQ Sequence 166 AA;

Query Match 54.9%; Score 179.5; DB 15; Length 166;

Best Local Similarity 49.2%; Pred. No. 2.4e-11;

Matches 31; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

Qy 2 QEPVKGP-----VSTKPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGCGMACF 54

Db 104 QDPVKAQPAVPGRFLLSKRGHCPRILFRCLPSNPSNKCWRDYDCPGVKKCCGCGKDC 163

Qy 55 VPQ 57

Db 164 YPK 166

RESULT 11

AAR50334

ID AAR50334 standard; Protein; 189 AA.

XX

AC AAR50334;

XX

DT 17-OCT-1994 (first entry)

XX

DE SPAI peptide.

XX

KW SPAI; sodium ion, potassium ion, ATP-ase inhibitor peptide; cardiac;

XW vascular disease; PCR; polymerase chain reaction.

XX

OS Sus scrofa.

XX

PN JP06049098-A.

XX

PD 22-FEB-1994.

XX

PF 29-JUL-1992; 92JP-0202286.

XX

PR 29-JUL-1992; 92JP-0202286.

XX

PA (EISA) EISAI CO LTD.

XX

DR WPI; 1994-097819/12.

DR P-PSDB; AAR50334.

XX

PT Sodium ion, potassium ion ATP-ase inhibitor peptide and corresp.

PT DNA - useful to treat cardiac and vascular disease

XX

PS Claim 1; Page 6-7; 8pp; Japanese.

XX

CC The sequence (AAQ44862) encodes the SPAI peptide which is useful

CC as a drug for treating cardiac and vascular diseases. The peptide

CC is found as a pre-sequence (AAR50335) which is amplified using

CC primers (AAQ44863-67)

XX

SQ Sequence 189 AA;

Query Match 54.9%; Score 179.5; DB 15; Length 189;

Best Local Similarity 49.2%; Pred. No. 2.8e-11;

Matches 31; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

Qy ' 2 QEPVKGP-----VSTKPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGCGMACF 54

Db 104 QDPVKAQPAVPGRFLLSKRGHCPRILFRCLPSNPSNKCWRDYDCPGVKKCCGCGKDC 163

Db 127 QDPVKAQPAVPGRFLLSKRGHCPRILFRCLPSNPSNKCWRDYDCPGVKKCCGCGKDC 186

Qy 55 VPQ 57

Db 187 YPK 189

RESULT 12

AAR08145

ID AAR08145 standard; protein; 61 AA.

XX

AC AAR08145;

XX

DT 01-MAR-1991 (first entry)

XX

DE Generic sodium potassium ATPase inhibiting peptide.

XX

KW Na,K-ATPase.

XX

OS Sus scrofa domestica.

XX

FH Key Location/Qualifiers

FT Misc-difference 22

FT /label= Arg or Gly

FT /note= "R when AA 30 = S, G when AA 30 = G"

FT Misc-difference 30

FT /label= Ser or Gly

FT /note= "S when AA 22 = R, G when AA 22 = G"

XX

PN JP02264797-A.

XX

PD 29-OCT-1990.

XX

PF 05-APR-1989; 89JP-0086073.

XX

PR 05-APR-1989; 89JP-0086073.

XX

PA (EISA) EISAI KK.

XX

DR WPI; 1990-365921/49.

XX

PT Sodium potassium ATP inhibiting new peptide - has specified

PT sequence of 61 aminoacid(s)

XX

PS Claim 1; Page 1073; 10pp; Japanese.

XX

SQ Sequence 61 AA;

Query Match 54.3%; Score 177.5; DB 11; Length 61;

Best Local Similarity 53.4%; Pred. No. 1.5e-11;

Matches 31; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

Qy 1 AQEPVKGP-VSTKPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGCGMACFVPQ 57

Db 4 AQPAVPGRFLLSKRGHCPRILFRCLPSNPSNKCWRDYDCPGVKKCCGCGKDC 61

RESULT 13

AAR08146

ID AAR08146 standard; protein; 61 AA.

XX

AC AAR08146;

XX

DT 01-MAR-1991 (first entry)

XX

DE Sodium potassium ATPase inhibiting peptide.

XX

KW Na,K-ATPase.

XX

OS Sus scrofa domestica.

XX

PN JP02264797-A.

PD 29-OCT-1990.
XX
PF 05-APR-1989; 89JP-0086073.
XX
PR 05-APR-1989; 89JP-0086073.
XX
PA (EISA) EISAI KK.
XX
DR WPI; 1990-365921/49.
XX
PT Sodium potassium ATP inhibiting new peptide - has specified
PT sequence of 61 aminoacid(s)
XX
PS Disclosure; Fig 2; 10pp; Japanese.
XX
SQ Sequence 61 AA;

Query Match 53.4%; Score 174.5; DB 11; Length 61;
Best Local Similarity 53.4%; Pred. No. 3.2e-11;
Matches 31; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

QY 1 AQEPVKGP-VSTKPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVPQ 57
Db 4 AQPAVPGRFLLSKRGHCPRIILFRCLPSNPNKWCWRYDCPGVKKCCGFCGKDCLYPK 61

RESULT 14
AAB92379
ID AAB92379 standard; Peptide; 49 AA.
AC AAB92379;
XX
DT 22-JUN-2001 (first entry)
XX
DE Miscellaneous peptide SEQ ID NO:1555.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
PS Disclosure; Page 713; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 49 AA;

Query Match 52.6%; Score 172; DB 22; Length 49;
Best Local Similarity 57.4%; Pred. No. 4.7e-11;
Matches 27; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 11 TKPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVPQ 57
Db 3 SKRGHCPRILFRCLPSNPNKWCWRYDCPGVKKCCGFCGKDCLYPK 49

RESULT 15
AAW98909
ID AAW98909 standard; Protein; 126 AA.
XX
AC AAW98909;
XX
DT 05-MAY-1999 (first entry)
XX
DE Mouse IMC carcinoma cell IMC-HA1 clone 28-1#3 protein #1.
XX
KW Mouse; carcinoma cell; IMC-HA1; cancer; metastasis; CMAP; inhibitor;
KW cancer metastasis associated protein.
XX
OS Mus musculus.
XX
PN WO9845431-A1.
XX
PD 15-OCT-1998.
XX
PF 07-APR-1998; 98WO-JP01592.
XX
PR 08-APR-1997; 97JP-0105333.
XX
PA (BANY) BANYU PHARM CO LTD.
XX
PI Arakawa H, Morita M, Ohta M;
XX
DR WPI; 1999-080732/07.
DR N-PSDB; AAX18516.
XX
PT Protein associated with cancer metastasis and gene encoding it -
PT useful for screening for potential inhibitors of cancer metastasis
XX
PS Claim 1; Page 47-48; 74pp; Japanese.
XX
CC The present invention provides gene sequences associated with cancer
CC metastasis which are isolated from mouse IMC carcinoma cells by
CC detection of their higher expression in IMC-HM cell lines than in
CC IMC-LM cell lines using differential display of the mRNA in these cells.
CC The gene sequences can be used for the screening of potential inhibitors
CC of cancer metastasis by either: bringing into contact with the cancer
CC metastasis associated protein (CMAP) and determining the degree of
CC binding; or creating a transformant cell line which expresses CMAP and
CC measuring the degree of expression of CMAP using an antibody recognising
CC the protein, either in the presence or absence of the potential
CC inhibitor. IMC-HM cells transformed with antisense CMAP DNA show a
CC lowered ability to metastasise. The present sequence represents a
CC specifically claimed protein sequence from the present invention.
XX
SQ Sequence 126 AA;

Query Match 49.2%; Score 161; DB 20; Length 126;

09-SEP-1993; 93WO-US08486.

```

09-SEP-1992; 92US-0943369.
(SYND ) SYNERGEN INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Eisenberg S, Thompson RC, Wahl SM;
WPI; 1994-118153/14.
Inhibiting retroviral infection with serine leucocyte protease
inhibitor - esp. for treating or preventing HIV infection, also
new protease inhibitors and nucleic acids encoding them
Claim 25; Page 17; 21pp; English.
Retroviral infection is inhibited by admin. of an SLPI, or its
analogue or deriv. A useful SLPI deriv. is CLPI, a truncated SLPI
mol. having only the last 60 amino acids of the native parotid
inhibitor. SLPI acts by blocking a host cell enzyme essential for
retroviral infection; it is a powerful inhibitor of human leucocyte
elastase, cathepsin G and human trypsin. The inhibitor provides an
effective and relatively safe method for treating HIV infections.
Sequence 60 AA;
Query Match 45.0%; Score 147; DB 15; Length 60;
Best Local Similarity 48.2%; Pred. No. 2.4e-08;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;
QY 3 EPVKGPVST--KPGSCPILIRCAMLNPPNRCLKDTCPGIKKCEGSCGMACFVP 56
Db :||| | | ||||| : ||||| | | ||||| : ||||| :|
2 DPVDTPTRRKPGKCPVTYGCVMNLNPPNFCMDGQCKRDLKCCMGCKSCVSP 57
RESULT 19
AAR51172
ID AAR51172 standard; Protein; 60 AA.
AC AAR51172;
XN
DT 26-OCT-1994 (first entry)
XX
DE CLPI.
KW Serine leucocyte protease inhibitor; SLPI; truncated SLPI; CLPI;
KW retrovirus; retroviral infection; HIV; parotid inhibitor; enzyme;
KW elastase; cathepsin G; trypsin.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 27 /note= "Leu encoded by CCT"
FT
XX
PN WO9406454-A.
XX
PD 31-MAR-1994.
XX
PF 09-SEP-1993; 93WO-US08486.
XX
PR 09-SEP-1992; 92US-0943369.
XX
PA (SYND ) SYNERGEN INC.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Eisenberg S, Thompson RC, Wahl SM;
XX
WPI; 1994-118153/14.
XX
N-PSDB; AAQ45442.
XX
Inhibiting retroviral infection with serine leucocyte protease
inhibitor - esp. for treating or preventing HIV infection, also
new protease inhibitors and nucleic acids encoding them

```

QY 3 BPVKGVPST--KPGSCPIILIRCAMLNPPNRCUKDTCPCGIIKKCCGSCGMACFVP 56
:| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 2 DPVDTPTRRKPGKCPVTYGCFCMLNPPNFCFMDGQCKRDLKCCMGMCCKSCVSP 57

RESULT 21

AAW01843
ID AAW01843 standard; peptide; 58 AA.

XX AC AAW01843;

XX DT 28-OCT-1997 (first entry)

XX DE Antileukoprotease derived tryptase clara inhibitor.

XX KW Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral;
KW respiratory tract; lung disease; respiratory syncytial virus; RSV;
KW influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
KW exosporium glycoprotein.

XX OS Homo sapiens.

XX PN WO9703694-A1.

XX PD 06-FEB-1997.

XX PF 24-JUL-1996; 96WO-JP02071.

XX PR 24-JUL-1995; 95JP-0186094.

XX PA (TANB) TOKYO TANABE CO.

XX PI Beppu Y, Imamura Y, Kido H, Tashiro M;

XX DR WPI; 1997-132378/12.

XX PT Tryptase clara inhibitor comprises anti-leuko:protease fragment -
PT useful for treatment and prevention of tryptase clara activated
PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
PT and measles

XX PS Claim 2; Page 20; 40pp; Japanese.

XX CC AAW01843-W01851 are peptides derived from the C-terminal portion of
CC human antileukoprotease. The peptides inhibit the action of tryptase
CC clara. Tryptase clara is responsible for the activation of viruses that
CC have exosporium glycoproteins, such as those that infect the respiratory
CC tract. The peptides are useful for the treatment and prevention of, for
CC example, influenza, parainfluenza, respiratory syncytial virus (RSV),
CC mumps and measles.

XX SQ Sequence 58 AA;

Query Match 43.7%; Score 143; DB 18; Length 58;
Best Local Similarity 47.2%; Pred. No. 6e-08;
Matches 25; Conservative 3; Mismatches 25; Indels 0; Gaps 0;

QY 4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCUKDTCPCGIIKKCCGSCGMACFVP 56

Db 3 PEFNPTRRKPGKCPVTYGCFCMLNPPNFCFMDGQCKRDLKCCMGMCCKSCVSP 55

RESULT 22

AAW01844
ID AAW01844 standard; peptide; 58 AA.

XX AC AAW01844;

XX DT 28-OCT-1997 (first entry)

XX DE Antileukoprotease derived tryptase clara inhibitor.

XX KW Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral;

KW respiratory tract; lung disease; respiratory syncytial virus; RSV;
KW influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
KW exosporium glycoprotein.

XX OS Homo sapiens.

XX PN WO9703694-A1.

XX PD 06-FEB-1997.

XX PF 24-JUL-1996; 96WO-JP02071.

XX PR 24-JUL-1995; 95JP-0186094.

XX PA (TANB) TOKYO TANABE CO.

XX PI Beppu Y, Imamura Y, Kido H, Tashiro M;

XX DR WPI; 1997-132378/12.

XX PT Tryptase clara inhibitor comprises anti-leuko:protease fragment -
PT useful for treatment and prevention of tryptase clara activated
PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
PT and measles

XX PS Claim 2; Page 20-21; 40pp; Japanese.

XX CC AAW01843-W01851 are peptides derived from the C-terminal portion of
CC human antileukoprotease. The peptides inhibit the action of tryptase
CC clara. Tryptase clara is responsible for the activation of viruses that
CC have exosporium glycoproteins, such as those that infect the respiratory
CC tract. The peptides are useful for the treatment and prevention of, for
CC example, influenza, parainfluenza, respiratory syncytial virus (RSV),
CC mumps and measles.

XX SQ Sequence 58 AA;

Query Match 43.7%; Score 143; DB 18; Length 58;
Best Local Similarity 47.2%; Pred. No. 6e-08;
Matches 25; Conservative 3; Mismatches 25; Indels 0; Gaps 0;

QY 4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCUKDTCPCGIIKKCCGSCGMACFVP 56

Db 3 PEFNPTRRKPGKCPVTYGCFCMLNPPNFCFMDGQCKRDLKCCMGMCCKSCVSP 55

RESULT 23

AAW53100

ID AAW53100 standard; Peptide; 60 AA.

XX AC AAW53100;

XX DT 27-FEB-2001 (first entry)

XX DE Serine protease inhibitor peptide sequence.

XX KW Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
KW protease mediated tissue destruction; emphysema; glomerulonephritis;
KW periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
KW elastase.

XX OS Synthetic.

XX PN US6132990-A.

XX PD 17-OCT-2000.

XX PF 07-JUN-1991; 91US-0712354.

XX PR 03-JAN-1989; 89US-0293042.

XX PR 06-DEC-1984; 84US-0678822.

XX PR 02-DEC-1985; 85US-0803471.

XX PR 29-JUL-1986; 86US-0890526.

PT the production of a serine protease inhibitor protein, e.g. leukocyte
PT elastase or trypsin -

XX Example 9; Column 42; 37pp; English.

PS The invention relates to a DNA sequence encoding an analog of a mammalian
CC serine protease inhibitor protein. The analog comprises at least eight
CC cysteine residues and possesses serine protease inhibitor activity, and
CC at least one operational element consisting of a promoter, an operator,
CC a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site
CC or a terminator codon. The DNA is useful in recombinant DNA techniques
CC for directing the production of a serine protease inhibitor protein,
CC e.g. leukocyte elastase or trypsin. The present sequence represents a
CC secretory leukocyte protease inhibitor (SLPI) analogue that has
CC chymotrypsin and elastase inhibitory activity.

XX Sequence 60 AA;

Query Match 43.7%; Score 143; DB 22; Length 60;
Best Local Similarity 48.2%; Pred. No. 6.2e-08;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSCGMACFVP 56
Db 2 DPVDTNPTRRKPGKCPVTYQGCLMLNPPNFCMDGQCKRDLKCCMGCMGKSCVSP 57

RESULT 26

AAP70583
ID AAP70583 standard; protein; 90 AA.

XX AAP70583;

XX 21-FEB-1991 (first entry)

XX Sequence of protein with the biological activity of HUSI
DE (human seminal plasma inhibitor) type I inhibitors encoded on PRH31.

XX Bronchitis therapy; cervix inflammation; hyperfibrinolysis.

XX Homo sapiens.

XX DE3600571-A.

XX 06-AUG-1987.

XX 10-JAN-1986; 86DE-3600571.

XX 10-JAN-1986; 86DE-3600571.

XX (CHEF) GRUNENTHAL GMBH.

XX Heinzl R, Appelhans H, Gassen HG, Machleidt W;

XX N-PSDB; AAN70929.

XX New protein with human seminal plasma inhibitor activity - and
PT new DNA coding sequences, vectors and transformed organisms,
PT useful eg for treating bronchitis or inflammation

PS Disclosure; Fig 4; 28pp; German.

XX HUSI-type inhibitors are useful for treating chronic bronchitis,
CC chronic cervical inflammation; inflammation associated with
CC excessive mucus prodn.; post-operative bleeding caused by
CC hyperfibrinolysis, or shock. They are esp. suitable for
CC administration as spray or inhalation. The expression control
CC sequence on the DNA fragment in AAN70928 is bound to the 5'-end of
CC HUSI cDNA in an expression vector.

XX Sequence 90 AA;

Query Match 43.7%; Score 143; DB 8; Length 90;
Best Local Similarity 48.2%; Pred. No. 9e-08;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSCGMACFVP 56
Db 32 DPVDTNPTRRKPGKCPVTYQGCLMLNPPNFCMDGQCKRDLKCCMGCMGKSCVSP 87

RESULT 27

AAB53102
ID AAB53102 standard; Peptide; 91 AA.

XX AAB53102;

XX 27-FEB-2001 (first entry)

XX Serine protease inhibitor analogue peptide sequence.

XX Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
KW protease mediated tissue destruction; emphysema; glomerulonephritis;
KW periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
KW elastase.

XX Synthetic.

XX US6132990-A.

XX 17-OCT-2000.

XX 07-JUN-1991; 91US-0712354.

XX 03-JAN-1989; 89US-0293042.

XX 06-DEC-1984; 84US-0678822.

XX 02-DEC-1985; 85US-0803471.

XX 29-JUL-1986; 86US-0890526.

XX 30-MAR-1987; 87US-0031846.

XX 04-AUG-1987; 87US-0082962.

XX (AMGE-) AMGEN BOULDER INC.

XX Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;

XX WPI; 2000-678667/66.

XX New serine protease inhibitors and DNA sequences for treating a
PT protease-mediated condition or tissue destruction e.g. emphysema or
PT tumor invasion and for recombinant production of inhibitors -

XX Claim 35; Column 65-66; 47pp; English.

XX This invention relates to new purified and isolated mammalian serine
CC protease inhibitor proteins which comprise at least 8 cysteine residues
CC and no more than 107 amino acids. The protease inhibitors are capable of
CC inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534,
CC AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the
CC protease inhibitors of the invention, and include oligonucleotide
CC sequences used in the isolation and characterisation of the proteins.
CC Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the
CC construction of DNA encoding the protease inhibitors. Peptide sequences
CC AAB53098 - AAB53122 represent the protease inhibitor of the invention and
CC various other peptides used in the isolation of the protease inhibitors.
CC The protease inhibitors have cytostatic and anti-inflammatory activity.
CC The serine protease inhibitor protein is useful for treating a
CC protease-mediated condition, which includes protease mediated tissue
CC destruction, e.g. emphysema, arthritis, glomerulonephritis,
CC periodontitis, muscular dystrophy or tumour invasion. It is also useful
CC for modulating protease activity. The DNAs are useful for producing the
CC proteins, especially by recombinant methods.

XX Sequence 91 AA;

Query Match 43.7%; Score 143; DB 21; Length 91;

Best Local Similarity 48.2%; Pred. No. 9.1e-08;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPILIRCAMLNPPNRCCLKDTPGIIKCCGSGCMACFVP 56
Db 33 DPVDTPNPTRRKPGKCPVTYQCLMLNPPNFCMDGQCKRDLKCCMGCGKSCVSP 88

RESULT 28

AAP82403
ID AAP82403 standard; protein; 106 AA.

XX AAP82403;

DT 07-NOV-1990 (first entry)

DE Serine protease inhibitor #2.

XX serine protease inhibitor; leukocyte elastase inhibitor.

PN US4760130-A.

PD 26-JUL-1988.

PF 02-DEC-1985; 85US-0803423.

PR 06-DEC-1984; 84US-0678823.

XX (SYNE-) SYNERGEN BIOLOGICAL.

PI Thompson RC, Ohlsson K;

XX WPI; 1988-227612/32.

PT New serine protease inhibitors -
PT isolated from parotid secretions.

PS Claim 10; Page 15; 9pp; English.

XX Single polypeptide chain protein with at least one active site
CC possessing serine protease inhibitor activity. The protein
CC is resistant to denaturation by heat and acids
CC and is resistant to proteolytic enzymes. It also has the
CC ability to refold following complete reduction of disulphide bonds
CC or denaturation of non-covalent interactions.
CC See also AAP82402 and AAP82597.

XX Sequence 106 AA;

Query Match 43.7%; Score 143; DB 9; Length 106;

Best Local Similarity 48.2%; Pred. No. 1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPILIRCAMLNPPNRCCLKDTPGIIKCCGSGCMACFVP 56
Db 49 DPVDTPNPTRRKPGKCPVTYQCLMLNPPNFCMDGQCKRDLKCCMGCGKSCVSP 104

RESULT 29

AAP60562
ID AAP60562 standard; protein; 107 AA.

XX AAP60562;

DT 01-JAN-1980 (first entry)

DE Synthetic protein capable of directing microbial synthesis of a
DE serine protease inhibitor having similar properties to protein
DE isolated from parotid secretions.

XX Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
KW trypsin-; inhibitor; ss.

OS Synthetic.

XX WO8603519-A.

XX 19-JUN-1986.

PF 04-DEC-1985; 85WO-US02385.

PR 04-DEC-1985; 85WO-US02385.

PR 06-DEC-1984; 84US-0678822.

PR 02-DEC-1985; 85US-0803471.

XX (SYNE-) SYNERGEN BIOLOG INC.

XX Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;

DR WPI; 1986-169458/26.

DR N-PSDB; AAN60463.

XX New synthetic DNA sequences for directing microbial synthesis -
PT for prodn. of single polypeptide chain serine protease inhibitor
PT having leukocyte elastase and trypsin inhibitory sites

XX Disclosure; Page 14; 59pp; English.

XX The protein directs synthesis of a single chain polypeptide serine
CC protease-inhibitor, which believed to have at least 2 active sites,
CC 1 exhibiting leukocyte-elastase-inhibiting properties and the other
CC exhibiting activity against trypsin. See also AAN60464-69 and AAP60562-
CC 66.

XX Sequence 107 AA;

Query Match 43.7%; Score 143; DB 7; Length 107;

Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPILIRCAMLNPPNRCCLKDTPGIIKCCGSGCMACFVP 56
Db 49 DPVDTPNPTRRKPGKCPVTYQCLMLNPPNFCMDGQCKRDLKCCMGCGKSCVSP 104

RESULT 30

AAP60563

ID AAP60563 standard; protein; 107 AA.

XX AAP60563;

DT 01-JAN-1980 (first entry)

XX Synthetic sequence capable of directing microbial synthesis of a
DE secretory leukocyte protease-inhibitor.

XX Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
KW trypsin-; inhibitor; ss.

XX Synthetic.

XX WO8603519-A.

XX 19-JUN-1986.

PF 04-DEC-1985; 85WO-US02385.

PR 04-DEC-1985; 85WO-US02385.

PR 06-DEC-1984; 84US-0678822.

PR 02-DEC-1985; 85US-0803471.

XX (SYNE-) SYNERGEN BIOLOG INC.

XX Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;

XX WPI; 1986-169458/26.

DR N-PSDB; AAN60464.
XX
PT New synthetic DNA sequences for directing microbial synthesis -
PT for prodn. of single poly:peptide chain serine protease inhibitor
PT having leukocyte elastase and trypsin inhibitory sites
XX
PS Disclosure; Page 15; 59pp; English.
XX
CC The sequence directs synthesis of a secretory leukocyte protease-
CC inhibitor. See also AAN60463, AAN60465-69 and AAP60562, AAP60564-66.
XX
SQ Sequence 107 AA;

Query Match 43.7%; Score 143; DB 7; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 49 DPVDTNPTRRRKPGKCPVTYGCCLMLNPPNFCMDGQCKRDLKCCMGCMCGKSCVSP 104

RESULT 31
AAP82597
ID AAP82597 standard; protein; 107 AA.
XX
AC AAP82597;
XX

DT 07-NOV-1990 (first entry)
XX
DE serine protease inhibitor #1.
XX
KW serine protease inhibitor; leukocyte elastase inhibitor.
XX
PN US4760130-A.
XX

PD 26-JUL-1988.
XX

PF 02-DEC-1985; 85US-0803423.
XX

PR 06-DEC-1984; 84US-0678823.
XX

PA (SYNE-) SYNERGEN BIOLOGICAL.
XX

PI Thompson RC, Ohlsson K;
XX

DR WPI; 1988-227612/32.
XX

PT New serine protease inhibitors -
PT isolated from parotid secretions.
XX

PS Claim 5; Page 15; 9pp; English.
XX

CC Single polypeptide chain protein with at least one active site
CC possessing serine protease inhibitor activity. The protein
CC is resistant to denaturation by heat and acids
CC and are resistant to proteolytic enzymes. It also has the
CC ability to refold following complete reduction of disulphide bonds
CC or denaturation of non-covalent interactions.
CC See also AAP82402 and AAP82403.
XX

SQ Sequence 107 AA;

Query Match 43.7%; Score 143; DB 9; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 49 DPVDTNPTRRRKPGKCPVTYGCCLMLNPPNFCMDGQCKRDLKCCMGCMCGKSCVSP 104

RESULT 32

AAP90384
ID AAP90384 standard; protein; 107 AA.
XX
AC AAP90384;
XX
DT 01-NOV-1989 (first entry)
XX
DE Human polymorphonuclear leukocyte elastase inhibiting protein.
XX
KW Elastase inhibitor;
KW human polymorphonuclear leukocyte elastase inhibiting protein.
XX
OS Homo sapiens.
XX
PN WO89062239-A.
XX
PD 13-JUL-1989.
XX
PF 28-DEC-1988; 88WO-JP01342.
XX
PR 28-DEC-1987; 87JP-0330219.
XX
PA (TEIJ) TEIJIN LTD.
XX
PI Sugiyama T, Kamimura T, Masuda K, Okada M, Ohtsuka E;
XX
DR WPI; 1989-220549/30.
XX

PT Elastase-inhibiting peptide of low serine protease-inhibiting activity
PT - contains C-terminal portion of human polymorphonuclear leukocyte
PT elastase inhibiting protein.
XX
PS Claim 1; page 43; 55pp; Japanese.
XX

CC The sequence is human polymorphonuclear leukocyte elastase inhibiting
CC protein (SLPI) primary sequence (SLPI is residues 55-107). SLPI has
CC much lower serine protease inhibiting activity. It can be used to
CC treat lung ascites tumours, chronic articular rheumatism, gum
CC inflammation, muscular atrophy, allergic lung disease and shock.
XX
SQ Sequence 107 AA;

Query Match 43.7%; Score 143; DB 10; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 49 DPVDTNPTRRRKPGKCPVTYGCCLMLNPPNFCMDGQCKRDLKCCMGCMCGKSCVSP 104

RESULT 33
AAY17426
ID AAY17426 standard; protein; 107 AA.
XX
AC AAY17426;
XX

DT 30-JUL-1999 (first entry)
XX

DE Human serine protease inhibitor.
XX

KW Human; leukocyte elastase inhibitor; parotid secretion; emphysema;
KW serine protease inhibitor; protease/protease inhibitor imbalance;
KW pulmonary disease; polymorphonuclear granulocyte protease.
XX
OS Homo sapiens.
XX

PN US5900400-A.
XX

PD 04-MAY-1999.
XX

PF 29-JUL-1994; 94US-0283477.
XX

PR 10-JUN-1988; 88US-0205372.
PR 06-DEC-1984; 84US-0678823.
PR 02-DEC-1985; 85US-0803423.
PR 10-SEP-1990; 90US-0581126.
PR 06-DEC-1991; 91US-0807769.
PR 29-JUL-1994; 94US-0283477.
XX (AMGE-) AMGEN INC.
PA
XX
XX Ohlsson K, Thompson RC;
PI
XX
XX WPI; 1999-346413/29.
DR
XX
XX New serine protease inhibitor protein used in the treatment of
PT emphysema
PT
XX
XX Claim 25; Column 17; 12pp; English.

PS The present invention describes a serine protease inhibitor protein

XX comprising a 108 amino acid sequence of formula (I): R1-Gly-Lys-Ser-Phe-
CC Lys-Ala-Gly-Val-Cys-Pro-Lys-Lys-Ser-Ala-Gln-Cys-Leu-R2-Tyr-Lys-Lys-
CC Pro-Glu-Cys-Gln-Ser-Asp-R10-Gln-Cys-Pro-Gly-Lys-Arg-Cys-Pro-Asp-
CC Thr-Cys-Gly-Ile-Lys-Cys-Leu-Asp-Pro-Val-Asp-Thr-Pro-Asn-Pro-Thr-Arg-Arg-
CC Lys-Pro-Gly-Lys-Cys-Pro-Val-Thr-R13-Gly-Gln-Cys-R8-R3-R9-Asn-Pro-Pro-
CC Asn-Phe-Cys-Glu-R4-Asp-Gly-Gln-Cys-Lys-Arg-R11-R12-Lys-Cys-R5-Gly-
CC R6-Cys-Gly-Lys-Ser-Cys-Val-Ser-Pro-Val-Lys-R7 where R1 = serine or
CC proline; R2-R6 = methionine, valine, alanine, phenylalanine, tyrosine,
CC tryptophan, lysine, glycine or arginine; R7 = alanine or proline; R8,
CC R9 = methionine, valine, alanine, phenylalanine, tyrosine, tryptophan,
CC lysine, leucine, glycine or arginine; R10 = leucine, lysine, glutamic
CC acid, glutamine or tryptophan; R11 = leucine, lysine, glutamine or
CC aspartic acid; R12 = leucine, lysine, glutamic acid or glutamine; R13 =
CC tyrosine, glutamic acid or aspartic acid; provided that at least one of
CC R10-R13 is a substituted residue as compared to parotid secretion-
CC derived serine protease inhibitor in which R10 is tryptophan, R11 is
CC aspartic acid, R12 is leucine, and R13 is tyrosine. (I) is used in the
CC treatment of pulmonary diseases involving protease/protease inhibitor
CC imbalance, preferably emphysema. (I) can be used in the treatment of
CC diseases mediated by polymorphonuclear granulocyte protease. The present
CC sequence represents a specifically claimed serine protease.

XX
SQ Sequence 107 AA;

Query Match 43.7%; Score 143; DB 20; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVP 56
Db 49 DPVDTPTNPTTRRKPKCPVTYGYQCLMLNPNFCEMDGQCKRDLKCCMGCMGKSCVSP 104

RESULT 34
AAB53101
ID AAB53101 standard; Peptide; 107 AA.
XX
AC AAB53101;

XX 27-FEB-2001 (first entry)

XX Serine protease inhibitor peptide sequence.

XX Serine protease inhibitor; cystostatic; anti-inflammatory; arthritis;
KW protease mediated tissue destruction; emphysema; glomerulonephritis;
KW periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
KW elastase.

XX Synthetic.

XX US6132990-A.

XX 17-OCT-2000.

XX

PF 07-JUN-1991; 91US-0712354.
XX
PR 03-JAN-1989; 89US-0293042.
PR 06-DEC-1984; 84US-0678822.
PR 02-DEC-1985; 85US-0803471.
PR 29-JUL-1986; 86US-0890526.
PR 30-MAR-1987; 87US-0031846.
PR 04-AUG-1987; 87US-0082962.
XX
XX (AMGE-) AMGEN BOULDER INC.

PA Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;

XX WPI; 2000-678667/66.

XX New serine protease inhibitors and DNA sequences for treating a

PT protease-mediated condition or tissue destruction e.g. emphysema or

XX tumor invasion and for recombinant production of inhibitors

XX Claim 23; Column 63; 47pp; English.

PS This invention relates to new purified and isolated mammalian serine
XX protease inhibitor proteins which comprise at least 8 cysteine residues
CC and no more than 107 amino acids. The protease inhibitors are capable of
CC inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534,
CC AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the
CC protease inhibitors of the invention, and include oligonucleotide
CC sequences used in the isolation and characterisation of the proteins.
CC Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the
CC construction of DNA encoding the protease inhibitors. Peptide sequences
CC AAB53098 - AAB53122 represent the protease inhibitor of the invention and
CC various other peptides used in the isolation of the protease inhibitors.
CC The protease inhibitors have cytostatic and anti-inflammatory activity.
CC The serine protease inhibitor protein is useful for treating a
CC protease-mediated condition, which includes protease mediated tissue
CC destruction, e.g. emphysema, arthritis, glomerulonephritis,
CC periodontitis, muscular dystrophy or tumour invasion. It is also useful
CC for modulating protease activity. The DNAs are useful for producing the
CC proteins, especially by recombinant methods.

XX
SQ Sequence 107 AA;

Query Match 43.7%; Score 143; DB 21; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVP 56
Db 49 DPVDTPTNPTTRRKPKCPVTYGYQCLMLNPNFCEMDGQCKRDLKCCMGCMGKSCVSP 104

RESULT 35
AAG65993
ID AAG65993 standard; Protein; 107 AA.
XX
AC AAG65993;

XX 11-FEB-2002 (first entry)

XX Recombinant serine protease inhibitor protein.

XX Serine protease inhibitor protein; recombinant; leukocyte elastase;
KW trypsin.

XX Homo sapiens.

XX US6291662-B1.

XX 18-SEP-2001.

XX 22-SEP-1998; 98US-0158085.

XX 30-MAR-1987; 87US-0031846.

PR

A non-inflammatory vector composition, comprising nucleic acids and anti-inflammatory compound, useful for treating inflammatory disorders,

This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha1-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease,

CC cystic fibrosis, otitis media, otitis external or HIV infection, or
CC for treating an individual suffering from or at risk for a disease or
CC disorder involving unwanted protease activity. The proteins are useful
CC for treating dermatological diseases such as atopic dermatitis, eczema
CC and psoriasis, in inflammatory responses to viral infection, and for
CC treating herpes infection, corneal or epidermal ulceration, chronic
CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
CC tumour metastasis and tumour angiogenesis, gastric ulceration,
CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
CC bacterial infection, Alzheimer's disease, hypertension and muscular
CC dystrophy. The present sequence represents the human secretory
CC leukoprotease inhibitor used to create the fusion protein of the
CC invention.
XX
SQ Sequence 107 AA;

Query Match 43.7%; Score 143; DB 23; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVP 56
Db 49 DPVDTPNPTRRKPGKCPVYGGQCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 104

RESULT 38
AAU75058
ID AAU75058 standard; Protein; 107 AA.
XX
AC AAU75058;
XX
DT 23-APR-2002 (first entry)
XX
DE Human seine protease inhibitor #1.
XX
KW Serine protease inhibitor; human; tumour invasion; macular dystrophy;
KW leukocyte elastase inhibitor; cathepsin G inhibitor; trypsin inhibitor;
KW pancreatic elastase inhibitor; emphysema; rheumatoid arthritis;
KW glomerulonephritis; periodontitis.
XX
OS Homo sapiens.
XX
XX US2001056180-A1.
PN
XX 27-DEC-2001.
PD
XX 12-JUN-2001; 2001US-0880529.
PF
XX 10-JUN-1988; 88US-0205372.
PR 10-SEP-1990; 90US-0581126.
PR 06-DEC-1991; 91US-0807769.
PR 29-JUL-1994; 94US-0283477.
PR 05-MAR-1999; 99US-0262828.
XX
PA (AMGE-) AMGEN INC.
XX
PI Thompson RC, Ohlsson K;
XX
XX WPI; 2002-121475/16.
DR
XX Purified serine protease inhibitor proteins isolated from parotid
PT secretions, useful for inhibiting leukocyte elastase, cathepsin G,
PT trypsin and/or pancreatic elastase -
XX
XX Example 3; Page 8; l1pp; English.
PS
XX This invention relates to a novel serine protease inhibitor protein
CC comprising a purified, single-polypeptide-chain protein having at least
CC one active site possessing serine protease inhibitor activity. The
CC protein of the invention has leukocyte elastase inhibitor, cathepsin G
CC inhibitor, trypsin inhibitor and pancreatic elastase inhibitor
CC activities. A disturbance of the protease/protease inhibitor balance
CC may lead to diseases associated with protease-mediated tissue

CC destruction such as emphysema, rheumatoid arthritis,
CC glomerulonephritis, periodontitis, macular dystrophy, and tumour
CC invasion. The invention also comprises analogues of the serine protease
CC inhibitors in which the amino acid sequence is varied so as to improve
CC the properties of the protein. These improvements include
CC resistance to oxidative inactivation, improved inhibition of pancreatic
CC elastase, improved inhibition of cathepsin G and trypsin. The
CC present sequence represents the generic serine protease inhibitor #1
XX protein sequence of the invention.
SQ Sequence 107 AA;

Query Match 43.7%; Score 143; DB 23; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVP 56
Db 49 DPVDTPNPTRRKPGKCPVYGGQCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 104

RESULT 39
AAU75061
ID AAU75061 standard; Protein; 107 AA.
XX
AC AAU75061;
XX
DT 23-APR-2002 (first entry)
XX
DE Human serine protease inhibitor generic sequence #3.
XX
KW Serine protease inhibitor; human; tumour invasion; macular dystrophy;
KW leukocyte elastase inhibitor; cathepsin G inhibitor; trypsin inhibitor;
KW pancreatic elastase inhibitor; emphysema; rheumatoid arthritis;
KW glomerulonephritis; periodontitis.
XX
OS Homo sapiens.
XX
XX US2001056180-A1.
PN
XX 27-DEC-2001.
PD
XX 12-JUN-2001; 2001US-0880529.
PF
XX 10-JUN-1988; 88US-0205372.
PR 10-SEP-1990; 90US-0581126.
PR 06-DEC-1991; 91US-0807769.
PR 29-JUL-1994; 94US-0283477.
PR 05-MAR-1999; 99US-0262828.
XX
PA (AMGE-) AMGEN INC.
XX
PI Thompson RC, Ohlsson K;
XX
XX WPI; 2002-121475/16.
DR
XX Purified serine protease inhibitor proteins isolated from parotid
PT secretions, useful for inhibiting leukocyte elastase, cathepsin G,
PT trypsin and/or pancreatic elastase -
XX
XX Claim 15; Page - ; l1pp; English.
PS
XX This invention relates to a novel serine protease inhibitor protein
CC comprising a purified, single-polypeptide-chain protein having at least
CC one active site possessing serine protease inhibitor activity. The
CC

CC protein of the invention has leukocyte elastase inhibitor, cathepsin G
CC inhibitor, trypsin inhibitor and pancreatic elastase inhibitor
CC activities. A disturbance of the protease/protease inhibitor balance
CC may lead to diseases associated with protease-mediated tissue
CC destruction such as emphysema, rheumatoid arthritis,
CC glomerulonephritis, periodontitis, macular dystrophy, and tumour
CC invasion. The invention also comprises analogues of the serine protease
CC inhibitors in which the amino acid sequence is varied so as to improve
CC the properties of the protein. These improvements include
CC resistance to oxidative inactivation, improved inhibition of pancreatic
CC elastase, improved inhibition of cathepsin G and trypsin. The
CC present sequence represents the generic human serine protease
CC inhibitor protein sequence #3 of the invention.
CC Note; This sequence is not shown in the specification but was created by
CC the indexer from the sequence shown in AAU75057 and the information
CC given in claim 15.

XX Sequence 107 AA;

Query Match 43.7%; Score 143; DB 23; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 49 DPVDTNPTRRKPGKCPVTYQCLMLNPPNFCEMDGQCKRDLKCCMGCMGKSCVSP 104

RESULT 40

AAB53105
ID AAB53105 standard; Peptide; 108 AA.

XX AC AAB53105;

XX DT 27-FEB-2001 (first entry)

XX DE Serine protease inhibitor peptide sequence.

XX KW Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
XX KW protease mediated tissue destruction; emphysema; glomerulonephritis;
XX KW periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
XX KW elastase.

XX OS Synthetic.

XX PN US6132990-A.

XX PD 17-OCT-2000.

XX PF 07-JUN-1991; 91US-0712354.

XX PR 03-JAN-1989; 89US-0293042.

XX PR 06-DEC-1984; 84US-0678822.

XX PR 02-DEC-1985; 85US-0803471.

XX PR 29-JUL-1986; 86US-0890526.

XX PR 30-MAR-1987; 87US-0031846.

XX PR 04-AUG-1987; 87US-0082962.

XX PA (AMGE-) AMGEN BOULDER INC.

XX PI Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;

XX WPI; 2000-678667/66.

XX DR New serine protease inhibitors and DNA sequences for treating a
XX PT protease-mediated condition or tissue destruction e.g. emphysema or
XX PT tumor invasion and for recombinant production of inhibitors
XX PS Claim 40; Column 67-68; 47pp; English.
XX CC This invention relates to new purified and isolated mammalian serine
XX CC protease inhibitor proteins which comprise at least 8 cysteine residues
XX CC and no more than 107 amino acids. The protease inhibitors are capable of

CC inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534,
CC AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the
CC protease inhibitors of the invention, and include oligonucleotide
CC sequences used in the isolation and characterisation of the proteins.
CC Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the
CC construction of DNA encoding the protease inhibitors. Peptide sequences
CC AAB53098 - AAB53122 represent the protease inhibitor of the invention and
CC various other peptides used in the isolation of the protease inhibitors.
CC The protease inhibitors have cytostatic and anti-inflammatory activity.
CC The serine protease inhibitor protein is useful for treating a
CC protease-mediated condition, which includes protease mediated tissue
CC destruction, e.g. emphysema, arthritis, glomerulonephritis,
CC periodontitis, muscular dystrophy or tumour invasion. It is also useful
CC for modulating protease activity. The DNAs are useful for producing the
CC proteins, especially by recombinant methods.

XX Sequence 108 AA;

Query Match 43.7%; Score 143; DB 21; Length 108;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFVP 56
Db 50 DPVDTNPTRRKPGKCPVTYQCLMLNPPNFCEMDGQCKRDLKCCMGCMGKSCVSP 105

RESULT 41

AAP70584
ID AAP70584 standard; Protein; 132 AA.

XX AC AAP70584;

XX DT 21-MAY-1991 (first entry)

XX DE Sequence of protein with the biological activity of HUSI
XX DE (human seminal plasma inhibitor) type I inhibitors encoded on prH 34.

XX KW Bronchitis therapy; cervix inflammation; hyperfibrinolysis.

XX OS Homo sapiens.

XX PN DE3600571-A.

XX PD 06-AUG-1987.

XX PF 10-JAN-1986; 86DE-3600571.

XX PR 10-JAN-1986; 86DE-3600571.

XX PA (CHEF) GRUNENTHAL GMBH.

XX PI Heinzel R, Appelhans H, Gassen HG, Machleidt W, Seemuller U;

XX WPI; 1987-222038/32.

XX DR N-PSDB; AAN70930.

XX PT New protein with human seminal plasma inhibitor activity - and
XX PT new DNA coding sequences, vectors and transformed organisms,
XX PT useful eg for treating bronchitis or inflammation

XX PS Claim 20; Fig 5; 28pp; German.

XX CC HUSI-type I inhibitors are useful for treating chronic bronchitis,
XX CC chronic cervical inflammation; inflammation associated with
XX CC excessive mucus prodn.; post-operative bleeding caused by
XX CC hyperfibrinolysis, and shock. They are esp. suitable for
XX CC administration as spray or inhalation. The expression control
XX CC sequence on the DNA fragment in AAN70928 is bound to the 5' end of
XX CC HUSI cDNA in an expression vector.

XX Sequence 132 AA;

Query Match 43.7%; Score 143; DB 8; Length 132;
Best Local Similarity 48.2%; Pred. No. 1.3e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSCGMACFVP 56
Db 74 DPVDTPNPTRRKPGKCPVTYQGCLMLNPPNFCMDGQCKRDLKCCMGCMGKSCVSP 129

RESULT 42
AAR84056
ID AAR84056 standard; Protein; 132 AA.
XX AAR84056;
DT 24-OCT-1996 (first entry)
DE Secretory leukocyte protease inhibitor.
XX Secretory leukocyte protease inhibitor; SLPI; N-terminus; proteolysis;
KW inhibitor; human; trypsin; vasoactive intestinal peptide; VIP; CGRP;
KW calcitonin gene-related peptide; peptide histidine-methionine; mammal;
KW PHM; mast cell; asthma; allergic rhinitis; therapy.
XX Homo sapiens.

OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..25
FT /note= "signal peptide"
FT Protein 26..132
FT /note= "secretory leukocyte protease inhibitor"

XX WO9608275-A1.
PN 21-MAR-1996.
PD 11-SEP-1995; 95WO-US11445.
XX 12-SEP-1994; 94US-0304051.
PA (FARB) BAYER CORP.

PI Brownell E, Delaria KA, Muller DK;
XX WPI; 1996-179729/18.
DR Use of secretory leukocyte protease inhibitor - as inhibitor of
PT trypsin for treating mast cell-mediated conditions such as asthma
PT and allergic rhinitis

XX Disclosure; Fig 9; 65pp; English.
PS This sequence represents the human secretory leukocyte protease
XX inhibitor (SLPI). SLPI is a potent inhibitor of the proteolytic activity
CC of trypsin. These trypsin inhibitors were identified by incubation
CC with a trypsin containing material and a trypsin substrate. The
CC mixture is then monitored for cleavage of the substrate over time. By
CC comparing the cleavage of the substrate in the presence and the absence
CC of the test substance determines as to whether the substance is a
CC trypsin inhibitor. The trypsin substrate used is preferably vasoactive
CC intestinal peptide (VIP), calcitonin gene-related peptide (CGRP) or
CC peptide histidine-methionine (PHM). Mast cell, or trypsin, mediated
CC conditions in a mammal can be treated by administering an active fragment
CC of SLPI or a mutein (such as AAR84055) to the mammal. These conditions
XX include asthma and allergic rhinitis.

SQ Sequence 132 AA;
Query Match 43.7%; Score 143; DB 17; Length 132;
Best Local Similarity 48.2%; Pred. No. 1.3e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSCGMACFVP 56

Db 74 DPVDTPNPTRRKPGKCPVTYQGCLMLNPPNFCMDGQCKRDLKCCMGCMGKSCVSP 129
RESULT 43
ABB50282
ID ABB50282 standard; Protein; 132 AA.
XX ABB50282;
AC ABB50282;
XX 11-FEB-2002 (first entry)
DT Leukocyte protease inhibitor ovarian tumour marker protein, #54.
DE Ovarian tumour marker gene; human; overexpression; upregulation;
XX epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
KW identification; serous cystadenoma; borderline serous tumour;
KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
KW immune response pathway; cell proliferation regulation; protein folding;
KW membrane localised; secreted; therapeutic target; cytostatic;
KW gene therapy; vaccine.

XX Homo sapiens.

OS WO200175177-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US10947.

XX 03-APR-2000; 2000US-194336P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;

XX WPI; 2001-626450/72.

XX N-PSDB; ABA83108.

XX Detecting and identifying ovarian tumor, identifying increased risk for
PT developing ovarian cancer, and determining effectiveness of ovarian
PT cancer treatment, by measuring expression level of ovarian tumor marker
PT gene -

XX Claim 23; Page 98; 140pp; English.

XX The invention relates to methods for diagnosing and prognosing ovarian
CC tumors in an individual via the detection and measurement of the
CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,
CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
CC ABA83181 and ABA83183). The methods of the invention are useful for
CC detecting an ovarian tumour in a patient, for identifying an individual
CC at increased risk for developing ovarian cancer, in prognostic tests for
CC assessing the relative severity of ovarian cancer, in tests for
CC monitoring a patient in remission from ovarian cancer and in tests for
CC monitoring disease status in a patient being treated for ovarian cancer.
CC The methods can additionally be used to identify a particular tumour as
CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
CC mucinous cystadenoma, endometrioid carcinoma, undifferentiated carcinoma,
CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
CC tumour. The ovarian tumour marker genes of the invention were identified
CC using SAGE (serial analysis of gene expression) and were found to be
CC overexpressed in a broad variety of ovarian epithelial tumour cells
CC relative to normal ovarian epithelial cells. The marker genes are
CC implicated in immune response pathways, in the regulation of cell
CC proliferation and in protein folding, and many of these are membrane-
CC localised or secreted. In addition to their use as diagnostic and
CC prognostic markers, the ovarian tumour marker genes or their encoded

XX SQ Sequence 107 AA;

Query Match 43.4%; Score 142; DB 20; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.3e-07;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

OY 3 EPVKGPIVST--KPGSCPIILIRCAMLNPPNRCCLKDTCPIKKCCGSCGMACFVP 56
Db 49 DPVDTNPNTTRRKPGKCPVTYQGCLMLNPPNFCGMDGQCKRDLKCCMGCMGKSCVSP 104

RESULT 50
AAP90126
ID AAP90126 standard; protein; 53 AA.
XX AC AAP90126;
XX DT 01-NOV-1989 (first entry)
XX DE Human polymorphonuclear leukocyte elastase inhibiting protein.
XX KW Elastase inhibitor;
XX KW human polymorphonuclear leukocyte elastase inhibiting protein.
XX OS Homo sapiens.
XX PN WO8906239-A.
XX PD 13-JUL-1989.
XX PF 28-DEC-1988; 88WO-JP01342.
XX PR 28-DEC-1987; 87JP-0330219.
XX PA (TEIJ) TEIJIN LTD.
XX PI Sugiyama T, Kamimura T, Masuda K, Okada M, Ohtsuka E;
XX WPI; 1989-220549/30.
XX DR N-PSDB; AAN90354.
XX PT Elastase-inhibiting peptide of low serine protease-inhibiting activity
PT - contains C-terminal portion of human polymorphonuclear leukocyte
PT elastase inhibiting protein.
XX PS Disclosure; fig 2; 59pp; Japanese.
XX CC The sequence is a fragment of human polymorphonuclear leukocyte
CC elastase inhibiting protein (Asn 55-Ala 107). See AAN90354 for
CC nucleotide sequence. See also AAP90384.
XX SQ Sequence 53 AA;

Query Match 43.1%; Score 141; DB 10; Length 53;
Best Local Similarity 49.0%; Pred. No. 8.9e-08;
Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;

OY 8 PVSTKPGSCPIILIRCAMLNPPNRCCLKDTCPIKKCCGSCGMACFVP 56
Db 2 PTRRKPGKCPVTYQGCLMLNPPNFCGMDGQCKRDLKCCMGCMGKSCVSP 50

RESULT 51
AAR20553
ID AAR20553 standard; peptide; 53 AA.
XX AC AAR20553;
XX DT 24-APR-1992 (first entry)
XX DE SLPI C-terminal.
XX

KW Secretary leukocyte protease inhibitor; antibody; Ab; immunoassay;
KW neutrophil; elastase; diagnosis.
XX OS Homo sapiens.
XX PN JP03279862-A.
XX PD 11-DEC-1991.
XX PF 29-MAR-1990; 90JP-0081591.
XX PR 29-MAR-1990; 90JP-0081591.
XX (TEIJ) TEIJIN KK.
XX WPI; 1992-035310/05.
XX PT New anti-human secretory leucocyte protease inhibitor antibody -
PT recognises peptide with neutrophil elastase inhibiting activity,
PT for diagnosis and treatment of inflammatory diseases e.g. lung
PT disease
XX PS Claim 1; Page 1; 9pp; Japanese.
XX CC An anti-human SLPI antibody specific to the C-terminal of human SPLI
CC was prepd. SPLI has neutrophil elastase inhibiting activity.
CC The C-terminal comprises amino acids 55-107 of SPLI.
CC The antibody may be used in an immunoassay for the diagnosis and
CC the treatment of inflammatory diseases, esp. lung diseases.
XX SQ Sequence 53 AA;

Query Match 43.1%; Score 141; DB 13; Length 53;
Best Local Similarity 49.0%; Pred. No. 8.9e-08;
Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;

OY 8 PVSTKPGSCPIILIRCAMLNPPNRCCLKDTCPIKKCCGSCGMACFVP 56
Db 2 PTRRKPGKCPVTYQGCLMLNPPNFCGMDGQCKRDLKCCMGCMGKSCVSP 50

RESULT 52
AAR22029
ID AAR22029 standard; peptide; 53 AA.
XX AC AAR22029;
XX DT 13-JUL-1992 (first entry)
XX DE Elastase inhibiting peptide.
XX KW Disulphidation; reproducible; high yield.
XX OS Synthetic.
XX PN JP04036191-A.
XX PD 06-FEB-1992.
XX PF 01-JUN-1990; 90JP-0141523.
XX PR 01-JUN-1990; 90JP-0141523.
XX (TEIJ) TEIJIN KK.
XX WPI; 1992-092898/12.
XX PT Active esterase inhibiting active polypeptide prepn. - by
PT sulphonating inactive esterase and di:sulphiding sulpho deriv.
PT for simple high yield prodn. and reproduction
XX PS Claim 1; Page 1; 10pp; Japanese.
XX

CC The active elastase inhibiting polypeptide was prepd. by
CC sulphating inactive elastase inhibiting polypeptide obtd. by
CC genetic engineering, and direct disulphidation of the obtd. sulpho-
CC derivative without passing through the thiol deriv. stage. The
CC active elastase inhibiting polypeptide has an activity ratio for
CC trypsin inhibiting activity against elastase inhibitory activity of
CC at least 1,000. The active elastase inhibiting polypeptide may be
CC produced in high yield and with good reducibility.
XX
SQ Sequence 53 AA;

Query Match 43.1%; Score 141; DB 13; Length 53;
Best Local Similarity 49.0%; Pred. No. 8.9e-08;
Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;

QY 8 PVSTKPGSCPILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGMACFVP 56
Db 2 PTRRKPGKCPVITYGQCLMLNPPNFCFCEMDGQCKRDLKCCMGCMGKSCVSP 50

RESULT 53
AAR30482
ID AAR30482 standard; protein; 53 AA.
XX
AC AAR30482;
XX
DT 06-MAY-1993 (first entry)
XX
DE Blood coagulation inhibitor polypeptide.
XX
KW Cathepsin G activity; inhibitor; platelet aggregation;
KW serotonin release; secretory leukocyte protease inhibitor.
XX
OS Synthetic.
XX
PN JP04334325-A.
XX
PD 20-NOV-1992.
XX
PF 10-MAY-1991; 91JP-0105809.
XX
PR 10-MAY-1991; 91JP-0105809.
XX
PA (TEIJ) TEIJIN LTD.
XX
DR WPI; 1993-005502/01.
XX
PT Blood coagulation inhibitor, inhibits cathepsin G activity and
PT release of serotonin - useful in anti-platelet aggregation or
PT anti-thrombus drugs.
XX
PS Claim 1; Page 4; 5pp; Japanese.
XX
CC The polypeptide corresponds to amino acids Asn55-Ala107 of secretory
CC leukocyte protease inhibitor (SLPI). It is used as the active
CC component of a blood coagulation inhibitor which has cathepsin G
CC inhibiting activity. It inhibits platelet aggregation through
CC inhibition of cathepsin G and release of serotonin and may be used
CC in anti-platelet aggregation or anti-thrombus drugs.
XX
SQ Sequence 53 AA;

Query Match 43.1%; Score 141; DB 14; Length 53;
Best Local Similarity 49.0%; Pred. No. 8.9e-08;
Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;

QY 8 PVSTKPGSCPILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGMACFVP 56
Db 2 PTRRKPGKCPVITYGQCLMLNPPNFCFCEMDGQCKRDLKCCMGCMGKSCVSP 50

RESULT 54
AAW01847

ID AAW01847 standard; peptide; 53 AA.
XX
AC AAW01847;
XX
DT 28-OCT-1997 (first entry)
XX
DE Antileukoprotease derived tryptase clara inhibitor.
XX
KW Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral;
KW respiratory tract; lung disease; respiratory syncytial virus; RSV;
KW influenza; Haemophilus influenzae; mumps; paramyxovirus;
KW exosporium glycoprotein.
XX
OS Homo sapiens.
XX
PN WO9703694-A1.
XX
PD 06-FEB-1997.
XX
PF 24-JUL-1996; 96WO-JP02071.
XX
PR 24-JUL-1995; 95JP-0186094.
XX
PA (TANB) TOKYO TANABE CO.
XX
PI Beppu Y, Imamura Y, Kido H, Tashiro M;
XX
DR WPI; 1997-132378/12.
XX
PT Tryptase clara inhibitor comprises anti-leuko:protease fragment -
PT useful for treatment and prevention of tryptase clara activated
PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
PT and measles
XX
PS Claim 2; Page 22; 40pp; Japanese.
XX
CC AAW01843-W01851 are peptides derived from the C-terminal portion of
CC human antileukoprotease. The peptides inhibit the action of tryptase
CC clara. Tryptase clara is responsible for the activation of viruses that
CC have exosporium glycoproteins, such as those that infect the respiratory
CC tract. The peptides are useful for the treatment and prevention of, for
CC example, influenza, parainfluenza, respiratory syncytial virus (RSV),
CC mumps and measles.
XX
SQ Sequence 53 AA;

Query Match 43.1%; Score 141; DB 18; Length 53;
Best Local Similarity 49.0%; Pred. No. 8.9e-08;
Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;

QY 8 PVSTKPGSCPILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGMACFVP 56
Db 2 PTRRKPGKCPVITYGQCLMLNPPNFCFCEMDGQCKRDLKCCMGCMGKSCVSP 50

RESULT 55
AAW01850
ID AAW01850 standard; peptide; 53 AA.
XX
AC AAW01850;
XX
DT 28-OCT-1997 (first entry)
XX
DE Antileukoprotease derived tryptase clara inhibitor.
XX
KW Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral;
KW respiratory tract; lung disease; respiratory syncytial virus; RSV;
KW influenza; Haemophilus influenzae; mumps; paramyxovirus;
KW exosporium glycoprotein.
XX
OS Homo sapiens.
XX
PN WO9703694-A1.

XX 06-FEB-1997.
XX 24-JUL-1996; 96WO-JP02071.
XX 24-JUL-1995; 95JP-0186094.
XX (TANB) TOKYO TANABE CO.
XX Beppu Y, Imamura Y, Kido H, Tashiro M;
XX WPI; 1997-132378/12.
XX Tryptase clara inhibitor comprises anti:leuko:protease fragment -
PT useful for treatment and prevention of tryptase clara activated
PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
PT and measles
XX Claim 2; Page 24; 40pp; Japanese.
XX AAW01843-W01851 are peptides derived from the C-terminal portion of
CC human antileukoprotease. The peptides inhibit the action of tryptase
CC clara. Tryptase clara is responsible for the activation of viruses that
CC have exosporium glycoproteins, such as those that infect the respiratory
CC tract. The peptides are useful for the treatment and prevention of, for
CC example, influenza, parainfluenza, respiratory syncytial virus (RSV),
CC mumps and measles.
XX SQ Sequence 53 AA;
Query Match 43.1%; Score 141; DB 18; Length 53;
Best Local Similarity 49.0%; Pred. No. 8.9e-08;
Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;
QY 8 PVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVP 56
| | | | | : | | | | | | | | | | | | | | | | : | |
Db 2 PTRRKPGKCPVTYGGQCRMLNPPNFCMDGQCKRDLKCCMGCMGKSCVSP 50
RESULT 56
AAB53103
ID AAB53103 standard; Peptide; 57 AA.
XX AC AAB53103;
XX 27-FEB-2001 (first entry)
XX Serine protease inhibitor analogue peptide sequence.
DE Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
KW protease mediated tissue destruction; emphysema; glomerulonephritis;
KW periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
KW elastase.
XX OS Synthetic.
XX PN US6132990-A.
XX 17-OCT-2000.
XX 07-JUN-1991; 91US-0712354.
XX 03-JAN-1989; 89US-0293042.
PR 06-DEC-1984; 84US-0678822.
PR 02-DEC-1985; 85US-0803471.
PR 29-JUL-1986; 86US-0890526.
PR 30-MAR-1987; 87US-0031846.
PR 04-AUG-1987; 87US-0082962.
XX (AMGE-) AMGEN BOULDER INC.
PA Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
PI
XX

DR WPI; 2000-678667/66.
XX New serine protease inhibitors and DNA sequences for treating a
PT protease-mediated condition or tissue destruction e.g. emphysema or
PT tumor invasion and for recombinant production of inhibitors -
XX Claim 36; Column 65-66; 47pp; English.
XX This invention relates to new purified and isolated mammalian serine
CC protease inhibitor proteins which comprise at least 8 cysteine residues
CC and no more than 107 amino acids. The protease inhibitors are capable of
CC inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534,
CC AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the
CC protease inhibitors of the invention, and include oligonucleotide
CC sequences used in the isolation and characterisation of the proteins.
CC Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the
CC construction of DNA encoding the protease inhibitors. Peptide sequences
CC AAB53098 - AAB53122 represent the protease inhibitor of the invention and
CC various other peptides used in the isolation of the protease inhibitors.
CC The protease inhibitors have cytostatic and anti-inflammatory activity.
CC The serine protease inhibitor protein is useful for treating a
CC protease-mediated condition, which includes protease mediated tissue
CC destruction, e.g. emphysema, arthritis, glomerulonephritis,
CC periodontitis, muscular dystrophy or tumour invasion. It is also useful
CC for modulating protease activity. The DNAs are useful for producing the
CC proteins, especially by recombinant methods.
XX SQ Sequence 57 AA;
Query Match 43.1%; Score 141; DB 21; Length 57;
Best Local Similarity 49.0%; Pred. No. 9.5e-08;
Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;
QY 8 PVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCEGSCGMACFVP 56
| | | | | : | | | | | | | | | | | | | | | | : | |
Db 6 PTRRKPGKCPVTYGGQCLMLNPPNFCMDGQCKRDLKCCMGCMGKSCVSP 54
RESULT 57
AAW01851
ID AAW01851 standard; peptide; 58 AA.
XX AC AAW01851;
XX 28-OCT-1997 (first entry)
XX Antileukoprotease derived tryptase clara inhibitor.
DE Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral;
KW respiratory tract; lung disease; respiratory syncytial virus; RSV;
KW influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
KW exosporium glycoprotein.
XX OS Homo sapiens.
XX PN WO9703694-A1.
XX 06-FEB-1997.
XX 24-JUL-1996; 96WO-JP02071.
XX 24-JUL-1995; 95JP-0186094.
XX (TANB) TOKYO TANABE CO.
XX Beppu Y, Imamura Y, Kido H, Tashiro M;
XX WPI; 1997-132378/12.
XX Tryptase clara inhibitor comprises anti:leuko:protease fragment -
PT useful for treatment and prevention of tryptase clara activated
PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
PT and measles
PT

```

QY 4 PVKGPVSTKPGSCPILLIRCAMLNPPNRCCLKDTPGIIKKCCGSCGMACFVP 56
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 PEFNPTRRKPGKCPVTYGCRLNPPNFCEMDGQCKRDLKCCMGMCCKSCVSP 55
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 59
AAW01846
ID AAW01846 standard; peptide; 58 AA.
XX
AC AAW01846;
XX
XX 28-OCT-1997 (first entry)
XX
DE Antileukoprotease derived tryptase clara inhibitor.
XX
KW Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral;
KW respiratory tract; lung disease; respiratory syncytial virus; RSV;
KW influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
KW exosporium glycoprotein.
XX
OS Homo sapiens.
XX
PN WO9703694-A1.
XX
PD 06-FEB-1997.
XX
PF 24-JUL-1996; 96WO-JP02071.
XX
PR 24-JUL-1995; 95JP-0186094.
XX
PA (TANB ) TOKYO TANABE CO.
XX
PI Beppu Y, Imamura Y, Kido H, Tashiro M;
XX
DR WPI; 1997-132378/12.
XX
PT Tryptase clara inhibitor comprises anti-leuko:protease fragment -
PT useful for treatment and prevention of tryptase clara activated
PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
PT and measles
XX
PS Claim 2; Page 22; 40pp; Japanese.
XX
CC AAW01843-W01851 are peptides derived from the C-terminal portion of
CC human antileukoprotease. The peptides inhibit the action of tryptase
CC clara. Tryptase clara is responsible for the activation of viruses that
CC have exosporium glycoproteins, such as those that infect the respiratory
CC tract. The peptides are useful for the treatment and prevention of, for
CC example, influenza, parainfluenza, respiratory syncytial virus (RSV),
CC mumps and measles.
XX
SQ Sequence 58 AA;

Query Match 42.8%; Score 140; DB 18; Length 58;
Best Local Similarity 45.3%; Pred. No. 1.2e-07;
Matches 24; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

QY 4 PVKGPVSTKPGSCPILLIRCAMLNPPNRCCLKDTPGIIKKCCGSCGMACFVP 56
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 PEFNPTRRKPGKCPVTYGCRLNPPNFCEMDGQCKRDLKCCMGMCCKSCVSP 55
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 60
AAB47404
ID AAB47404 standard; protein; 107 AA.
XX
AC AAB47404;
XX
XX 19-SEP-2001 (first entry)
XX
DE SLPI oxidation-resistant mature form.
XX

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KW Secretory leukoprotease inactivator; SLPI; gene therapy;
KW antiprotease; lung; oxidation resistant; mutation;
KW chronic obstructive pulmonary disease; COPD.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Misc-difference 73
FT /label= M73L

XX WO200148231-A2.

XX 05-JUL-2001.

XX 27-DEC-2000; 2000WO-EPI3297.

XX 28-DEC-1999; 99US-0473018.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Lu P, Ennist DL, Mina M;

XX WPI; 2001-465212/50.

XX A non-inflammatory vector composition, comprising nucleic acids and
XX antiinflammatory compound, useful for treating inflammatory disorders,
XX e.g. rheumatoid arthritis, emphysema, cystic fibrosis, adult
XX respiratory distress syndrome and asthma -

XX Disclosure; Page 13; 30pp; English.

XX The sequences given in AAB47402-405 represent secretory leukoprotease
XX inactivator (SLPI) proteins which may be used in gene
XX therapy. SLPI is a major antiprotease present in the lung. A mutation
XX replacing Met73 of the mature protein with Leu renders the protein
XX oxidation resistant. Therefore it can be used to treat patients with
XX chronic obstructive pulmonary disease (COPD).

XX Sequence 107 AA;

Query Match 42.8%; Score 140; DB 22; Length 107;
Best Local Similarity 46.4%; Pred. No. 2.2e-07;
Matches 26; Conservative 5; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGVPST--KPGSCPILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGACFVP 56
Db 49 DPVDTNPTRRKPGKCPVYTGQCLLLNPPNFCMDGQCKRDLKCCMGCMGKSCVSP 104

RESULT 61

AAB47405

ID AAB47405 standard; protein; 132 AA.

XX AAB47405;

XX 19-SEP-2001 (first entry)

XX SLPI oxidation-resistant immature form.

XX Secretory leukoprotease inactivator; SLPI; gene therapy;
KW antiprotease; lung; oxidation resistant; mutation;
KW chronic obstructive pulmonary disease; COPD.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Misc-difference 98
FT /label= M73L

FT Peptide

FT 1..25

FT Protein

FT 26..132

FT /label= oxidation-resistant SLPI

XX WO200148231-A2.
XX 05-JUL-2001.
XX 27-DEC-2000; 2000WO-EPI3297.
XX 28-DEC-1999; 99US-0473018.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Lu P, Ennist DL, Mina M;
XX WPI; 2001-465212/50.

XX A non-inflammatory vector composition, comprising nucleic acids and
XX antiinflammatory compound, useful for treating inflammatory disorders,
XX e.g. rheumatoid arthritis, emphysema, cystic fibrosis, adult
XX respiratory distress syndrome and asthma -

XX Disclosure; Page 13; 30pp; English.

XX The sequences given in AAB47402-405 represent secretory leukoprotease
XX inactivator (SLPI) proteins which may be used in gene
XX therapy. SLPI is a major antiprotease present in the lung. A mutation
XX replacing Met73 of the mature protein with Leu renders the protein
XX oxidation resistant. Therefore it can be used to treat patients with
XX chronic obstructive pulmonary disease (COPD).

XX Sequence 132 AA;

Query Match 42.8%; Score 140; DB 22; Length 132;
Best Local Similarity 46.4%; Pred. No. 2.7e-07;
Matches 26; Conservative 5; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGVPST--KPGSCPILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGACFVP 56
Db 74 DPVDTNPTRRKPGKCPVYTGQCLLLNPPNFCMDGQCKRDLKCCMGCMGKSCVSP 129

RESULT 62

AAB53106

ID AAB53106 standard; Peptide; 101 AA.

XX AAB53106;

XX 27-FEB-2001 (first entry)

XX Human SLPI peptide sequence.

XX Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
KW protease mediated tissue destruction; emphysema; glomerulonephritis;
KW periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
KW elastase.

XX Homo sapiens.

XX US6132990-A.

XX 17-OCT-2000.

XX 07-JUN-1991; 91US-0712354.

XX 03-JAN-1989; 89US-0293042.

XX 06-DEC-1984; 84US-0678822.

XX 02-DEC-1985; 85US-0803471.

XX 29-JUL-1986; 86US-0890526.

XX 30-MAR-1987; 87US-0031846.

XX 04-AUG-1987; 87US-0082962.

XX (AMGE-) AMGEN BOULDER INC.

PI Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
XX
DR WPI; 2000-678667/66.
XX N-PSDB; AAC97530.
PT New serine protease inhibitors and DNA sequences for treating a
PT protease-mediated condition or tissue destruction e.g. emphysema or
PT tumor invasion and for recombinant production of inhibitors -
XX
PS Disclosure; Column 15-17; 47pp; English.
XX
CC This invention relates to new purified and isolated mammalian serine
CC protease inhibitor proteins which comprise at least 8 cysteine residues
CC and no more than 107 amino acids. The protease inhibitors are capable of
CC inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534,
CC AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the
CC protease inhibitors of the invention, and include oligonucleotide
CC sequences used in the isolation and characterisation of the proteins.
CC Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the
CC construction of DNA encoding the protease inhibitors. Peptide sequences
CC AAB53098 - AAB53122 represent the protease inhibitor of the invention and
CC various other peptides used in the isolation of the protease inhibitors.
CC The protease inhibitors have cytostatic and anti-inflammatory activity.
CC The serine protease inhibitor protein is useful for treating a
CC protease-mediated condition, which includes protease mediated tissue
CC destruction, e.g. emphysema, arthritis, glomerulonephritis,
CC periodontitis, muscular dystrophy or tumour invasion. It is also useful
CC for modulating protease activity. The DNAs are useful for producing the
CC proteins, especially by recombinant methods.
XX
SQ Sequence 101 AA;

Query Match 42.7%; Score 139.5; DB 21; Length 101;
Best Local Similarity 48.1%; Pred. No. 2.3e-07;
Matches 26; Conservative 3; Mismatches 20; Indels 5; Gaps 1;

QY 8 PVST-----KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCGCGMACFVP 56
||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| : |||
Db 46 PVDTPNPRRKPGKCPVTYGCCLMLNPPNFCEMDGQCKRDLKCCMGKSCVSP 99

RESULT 63
AAG65996
ID AAG65996 standard; Protein; 101 AA.
XX
AC AAG65996;

DT 11-FEB-2002 (first entry)
XX
XX Recombinant secretory leukocyte protease inhibitor (SLPI) protein.
DE Serine protease inhibitor protein; recombinant; leukocyte elastase;
XX trypsin; secretory leukocyte protease inhibitor; SLPI.
KW
XX Homo sapiens.
OS
XX US6291662-B1.
PN
XX 18-SEP-2001.
PD
XX 22-SEP-1998; 98US-0158085.
PF
XX 30-MAR-1987; 87US-0031846.
PR
XX 06-AUG-1990; 90US-0563832.
PR
XX 22-JUL-1994; 94US-0279056.
PR
XX 05-DEC-1984; 84US-0678222.
PR
XX 02-DEC-1985; 85US-0803471.
PR
XX 29-JUL-1986; 86US-0890526.
XX
PA (AMGE-) AMGEN INC.

PI Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
XX

DR WPI; 2001-637974/73.
DR N-PSDB; AAI67489, AAI67491.
XX
PT New DNA sequences, useful in recombinant DNA techniques for directing
PT the production of a serine protease inhibitor protein, e.g. leukocyte
PT elastase or trypsin -
XX
PS Disclosure; Columns 13-18; 37pp; English.
XX
CC The invention relates to a DNA sequence encoding an analog of a mammalian
CC serine protease inhibitor protein. The analog comprises at least eight
CC cysteine residues and possesses serine protease inhibitor activity, and
CC at least one operational element consisting of a promoter, an operator,
CC a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site
CC or a terminator codon. The DNA is useful in recombinant DNA techniques
CC for directing the production of a serine protease inhibitor protein,
CC e.g. leukocyte elastase or trypsin. The present sequence represents
CC a secretory leukocyte protease inhibitor (SLPI) protein.
XX
SQ Sequence 101 AA;

Query Match 42.7%; Score 139.5; DB 22; Length 101;
Best Local Similarity 48.1%; Pred. No. 2.3e-07;
Matches 26; Conservative 3; Mismatches 20; Indels 5; Gaps 1;

QY 8 PVST-----KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCGCGMACFVP 56
||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| : |||
Db 46 PVDTPNPRRKPGKCPVTYGCCLMLNPPNFCEMDGQCKRDLKCCMGKSCVSP 99

RESULT 64
AAW00663
ID AAW00663 standard; peptide; 98 AA.
XX
AC AAW00663;

DT 28-OCT-1996 (first entry)
XX
DE Mutein #1 of secretory leukocyte protease inhibitor residues 5-102.
XX
KW Secretory leukocyte protease inhibitor; SLPI; N-terminus; proteolysis;
KW inhibitor; human; tryptase; vasoactive intestinal peptide; VIP; CGRP;
KW calcitonin gene-related peptide; peptide histidine-methionine; mammal;
KW PHM; mast cell; asthma; allergic rhinitis; therapy.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Misc-difference 68
FT /note= "L72R"

XX WO9608275-A1.
XX 21-MAR-1996.
XX
XX 11-SEP-1995; 95WO-US11445.
XX
XX 12-SEP-1994; 94US-0304051.
XX
XX (FARB) BAYER CORP.

XX Brownell E, Delaria KA, Muller DK;
XX
XX WPI; 1996-179729/18.
XX
XX Use of secretory leukocyte protease inhibitor - as inhibitor of
XX trypsin for treating mast cell-mediated conditions such as asthma
XX and allergic rhinitis
XX
XX Claim 19; ; 65pp; English.

XX
XX AAR84055, and AAW00653-W00666 represent fragments and muteins of human
XX secretory leukocyte protease inhibitor (SLPI) (see AAR84056 for full

length wild type sequence). This sequence represents a Leu-72-Arg mutein of residues 5-102 of SLIP. SLPI is a potent inhibitor of the proteolytic activity of tryptase. These tryptase inhibitors were identified by incubation with a tryptase containing material and a tryptase substrate. The mixture is then monitored for cleavage of the substrate over time. By comparing the cleavage of the substrate as to whether presence and the absence of the test substance determines as to whether the substance is a tryptase inhibitor. The tryptase substrate used is preferably vasoactive intestinal peptide (VIP), calcitonin gene-related peptide (CGRP) or peptide histidine-methionine (PHM). Mast cell, or tryptase, mediated conditions in a mammal can be treated by administering an active fragment of SLPI (such as this sequence) or a mutein to the mammal. These conditions include asthma and allergic rhinitis.

Query Match 42.5%; Score 139; DB 17; Length 98;
Best Local Similarity 49.1%; Pred. No. 2.6e-07;
Matches 26; Conservative 4; Mismatches 21; Indels 2; Gaps 1;
Sequence 98 AA;

3 EPVKGPVST--KPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGCMAC 53
45 DPVDTNPNTRRKPGKCPVYTGQCRMLNPPNFCCEMDGQCKRDLKCCCMGCMGKSC 97

RESULT 65
AAW00664
ID AAW00664 standard; peptide; 98 AA.

AAW00664;

28-OCT-1996 (first entry)

Mutein #2 of secretory leukocyte protease inhibitor residues 5-102.

Secretory leukocyte protease inhibitor; SLPI; N-terminus; proteolysis; inhibitor; human; tryptase; vasoactive intestinal peptide; VIP; CGRP; calcitonin gene-related peptide; peptide histidine-methionine; mammal; PHM; mast cell; asthma; allergic rhinitis; therapy.

Synthetic.

Key Location/Qualifiers
Misc-difference 68 /note= "L72K"

WO9608275-A1.

21-MAR-1996.

11-SEP-1995; 95WO-US11445.

12-SEP-1994; 94US-0304051.

(FARB) BAYER CORP.

Brownell E, Delaria KA, Muller DK;

WPI; 1996-179729/18.

Use of secretory leukocyte protease inhibitor - as inhibitor of tryptase for treating mast cell-mediated conditions such as asthma and allergic rhinitis

Claim 19; ; 65pp; English.

AAR84055, and AAW00653-W00666 represent fragments and muteins of human secretory leukocyte protease inhibitor (SLPI) (see AAR84056 for full length wild type sequence). This sequence represents a Leu-72-Lys mutein of residues 5-102 of SLIP. SLPI is a potent inhibitor of the proteolytic activity of tryptase. These tryptase inhibitors were identified by incubation with a tryptase containing material and a tryptase substrate. The mixture is then monitored for cleavage of the

substrate over time. By comparing the cleavage of the substrate in the presence and the absence of the test substance determines as to whether the substance is a tryptase inhibitor. The tryptase substrate used is preferably vasoactive intestinal peptide (VIP), calcitonin gene-related peptide (CGRP) or peptide histidine-methionine (PHM). Mast cell, or tryptase, mediated conditions in a mammal can be treated by administering an active fragment of SLPI (such as this sequence) or a mutein to the mammal. These conditions include asthma and allergic rhinitis.

Sequence 98 AA;

Query Match 42.5%; Score 139; DB 17; Length 98;
Best Local Similarity 49.1%; Pred. No. 2.6e-07;
Matches 26; Conservative 4; Mismatches 21; Indels 2; Gaps 1;

3 EPVKGPVST--KPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGCMAC 53
45 DPVDTNPNTRRKPGKCPVYTGQCKMLNPPNFCCEMDGQCKRDLKCCCMGCMGKSC 97

RESULT 66
AAW00665
ID AAW00665 standard; peptide; 98 AA.

AAW00665;

28-OCT-1996 (first entry)

Mutein #3 of secretory leukocyte protease inhibitor residues 5-102.

Secretory leukocyte protease inhibitor; SLPI; N-terminus; proteolysis; inhibitor; human; tryptase; vasoactive intestinal peptide; VIP; CGRP; calcitonin gene-related peptide; peptide histidine-methionine; mammal; PHM; mast cell; asthma; allergic rhinitis; therapy.

Synthetic.

Key Location/Qualifiers
Misc-difference 15 /note= "L19R"

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21-MAR-1996.

11-SEP-1995; 95WO-US11445.

12-SEP-1994; 94US-0304051.

(FARB) BAYER CORP.

Brownell E, Delaria KA, Muller DK;

WPI; 1996-179729/18.

Use of secretory leukocyte protease inhibitor - as inhibitor of tryptase for treating mast cell-mediated conditions such as asthma and allergic rhinitis

Claim 19; ; 65pp; English.

AAR84055, and AAW00653-W00666 represent fragments and muteins of human secretory leukocyte protease inhibitor (SLPI) (see AAR84056 for full length wild type sequence). This sequence represents a Leu-19-Arg mutein of residues 5-102 of SLIP. SLPI is a potent inhibitor of the proteolytic activity of tryptase. These tryptase inhibitors were identified by incubation with a tryptase containing material and a tryptase substrate. The mixture is then monitored for cleavage of the substrate over time. By comparing the cleavage of the substrate in the presence and the absence of the test substance determines as to whether the substance is a tryptase inhibitor. The tryptase substrate used is preferably vasoactive intestinal peptide (VIP), calcitonin gene-related peptide (CGRP) or peptide histidine-methionine (PHM). Mast cell, or

RESULT 69
AAY17425
ID AAY17425 standard; protein; 107 AA.
XX
AC AAY17425;
XX
DT 30-JUL-1999 (first entry)
XX
DE Human serine protease inhibitor generic sequence.
XX
DE Human; leukocyte elastase inhibitor; parotid secretion; emphysema;
KW serine protease inhibitor; protease/protease inhibitor imbalance;
KW pulmonary disease; polymorphonuclear granulocyte protease.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /label= Ser, Pro
FT Misc-difference 20 /label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Arg
FT Misc-difference 30 /label= Leu, Glu, Gln, Trp
FT Misc-difference 68 /label= Tyr, Glu, Asp
FT Misc-difference 72 /label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Leu, Arg
FT Misc-difference 73 /label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Arg
FT Misc-difference 74 /label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Arg
FT Misc-difference 82 /label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Leu, Arg
FT Misc-difference 89 /label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Arg
FT Misc-difference 90 /label= Leu, Lys, Gln, Asp
FT Misc-difference 94 /label= Leu, Lys, Glu, Gln
FT Misc-difference 96 /label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Arg
FT Misc-difference 107 /label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Arg
FT /label= Ala, Pro
XX
PN US5900400-A.
XX
PD 04-MAY-1999.
XX
PF 29-JUL-1994; 94US-0283477.
XX
PR 10-JUN-1988; 88US-0205372.
PR 06-DEC-1984; 84US-0678823.
PR 02-DEC-1985; 85US-0803423.
PR 10-SEP-1990; 90US-0581126.
PR 06-DEC-1991; 91US-0807769.
PR 29-JUL-1994; 94US-0283477.
XX
PA (AMGE-) AMGEN INC.
XX
PI Ohlsson K, Thompson RC;
XX
DR WPI; 1999-346413/29.
XX
PT New serine protease inhibitor protein used in the treatment of
PT emphysema
XX
PS Claim 1; Column 15; 12pp; English.
XX
CC The present invention describes a serine protease inhibitor protein
comprising a 108 amino acid sequence of formula (I): R1-Gly-Lys-Ser-Phe-

Lys-Ala-Gly-Val-Cys-Pro-Lys-Lys-Ser-Ala-Gln-Cys-Leu-R2-Tyr-Lys-Lys-
Pro-Glu-Cys-Gln-Ser-Asp-R10-Gln-Cys-Pro-Gly-Lys-Lys-Arg-Cys-Pro-Asp-
Thr-Cys-Gly-Ile-Lys-Cys-Leu-Asp-Pro-Val-Asp-Thr-Pro-Asn-Pro-Thr-Arg-Arg-
Lys-Pro-Gly-Lys-Cys-Pro-Val-Thr-R13-Gly-Gln-Cys-R8-R3-R9-Asn-Pro-Pro-
Asn-Phe-Cys-Glu-R4-Asp-Gly-Gln-Cys-Lys-Arg-R11-R12-Lys-Cys-Cys-R5-Gly-
R6-Cys-Gly-Lys-Ser-Cys-Val-Ser-Pro-Val-Lys-R7 where R1 = serine or
proline; R2-R6 = methionine, valine, alanine, phenylalanine, tyrosine,
tryptophan, lysine, glycine or arginine; R7 = alanine or proline; R8,
R9 = methionine, valine, alanine, phenylalanine, tyrosine, tryptophan,
lysine, leucine, glycine or arginine; R10 = leucine, lysine, glutamic
acid, glutamine or tryptophan; R11 = leucine, lysine, glutamine or
aspartic acid; R12 = leucine, lysine, glutamic acid or glutamine; R13 =
tyrosine, glutamic acid or aspartic acid; provided that at least one of
R10-R13 is a substituted residue as compared to parotid secretion-
derived serine protease inhibitor in which R10 is tryptophan, R11 is
aspartic acid, R12 is leucine, and R13 is tyrosine. (I) is used in the
treatment of pulmonary diseases involving protease/protease inhibitor
imbalance, preferably emphysema. (I) can be used in the treatment of
diseases mediated by polymorphonuclear granulocyte protease.
XX
SQ Sequence 107 AA;
Query Match 42.2%; Score 138; DB 20; Length 107;
Best Local Similarity 44.6%; Pred. No. 3.5e-07;
Matches 25; Conservative 4; Mismatches 25; Indels 2; Gaps 1;
QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCCLKDTPGIIKKCCGSCMACFVP 56
Db 49 DPVDTNPTRRKPGKCPVTXGQCXXXNPPNFCEDGQCKRXXKCCXGCKSCVSP 104
RESULT 70
AAP60566
ID AAP60566 standard; protein; 49 AA.
XX
AC AAP60566;
XX
DT 01-JAN-1980 (first entry)
XX
DE Synthetic sequence capable of directing microbial synthesis of a
DE secretory leukocyte protease inhibitor.
XX
KW Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
KW trypsin-; inhibitor; ss.
XX
OS Synthetic.
XX
PN WO8603519-A.
XX
PD 19-JUN-1986.
XX
PF 04-DEC-1985; 85WO-US02385.
XX
PR 04-DEC-1985; 85WO-US02385.
PR 06-DEC-1984; 84US-0678822.
PR 02-DEC-1985; 85US-0803471.
XX
PA (SYNE-) SYNERGEN BIOLOG INC.
XX
PI Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
XX
DR WPI; 1986-169458/26.
DR N-PSDB; AAN60465.
XX
PT New synthetic DNA sequences for directing microbial synthesis -
PT for prodn. of single poly:peptide chain serine protease inhibitor
PT having leukocyte elastase and trypsin inhibitory sites
XX
PS Disclosure; Page 19; 59pp; English.
XX
CC This is the protein encoded by the second exon of AAN60465.
CC See also AAN60464, AAN60466-69 and AAP60562-65.
XX

SQ Sequence 49 AA;

Query Match 41.6%; Score 136; DB 7; Length 49;
Best Local Similarity 51.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 12 KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVP 56
||| ||| : ||| ||| | | | | | | | | : | |
Db 3 KPGKCPVTYQQCLMLNPPNFCCEMDGQCKRDLKCCMGCMCGKSCVSP 47

RESULT 71
AAR50084
ID AAR50084 standard; peptide; 49 AA.
XX
AC AAR50084;
XX
DT 24-NOV-1994 (first entry)
XX
DE Elastase-inhibiting peptide.
XX
KW Elastase; cathepsin G; neutrophil; inflammation; thrombosis;
KW inhibition; reperfusion; Secretory Leukoprotease Inhibitor;
KW SLPI; trypsin.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 6..35
FT Disulfide-bond 13..39
FT Disulfide-bond 22..34
FT Disulfide-bond 28..43
XX
PN JP06080697-A.
XX
PD 22-MAR-1994.
XX
PF 21-DEC-1992; 92JP-0340362.
XX
PR 24-DEC-1991; 91JP-0355553.
PR 17-JUL-1992; 92JP-0212398.
PR 17-JUL-1992; 92JP-0212399.
XX
PA (TEIJ) TEIJIN LTD.
XX
DR WPI; 1994-132044/16.
XX
PT Polypeptide(s) and fusion proteins inhibiting neutrophil elastase
PT and cathepsin G - useful to treat eg inflammation, thrombosis,
PT reperfusion, etc
XX
PS Claim 5; Page 24; 31pp; Japanese.
XX
CC Secretory Leukoprotease Inhibitor (SLPI) amino acids Arg59-Ala107
CC inhibits elastase and cathepsin G and does not inhibit trypsin. The
CC cpd. may be used for treating diseases associated with excessive
CC activation of the neutrophil or neutrophil-releasing protease, esp.
CC inflammation, platelet coagulation thrombosis and/or reperfusion
CC disorder after ischaemia.
XX
SQ Sequence 49 AA;

Query Match 41.6%; Score 136; DB 15; Length 49;
Best Local Similarity 51.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 12 KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVP 56
||| ||| : ||| ||| | | | | | | | | : | |
Db 2 KPGKCPVTYQQCLMLNPPNFCCEMDGQCKRDLKCCMGCMCGKSCVSP 46

RESULT 72
AAR58594

ID AAR58594 standard; protein; 49 AA.
XX
AC AAR58594;
XX
DT 09-MAY-1995 (first entry)
XX
DE Secretory leukocyte protease inhibitor derivative, Arg59-Ala107.
XX
KW Secretory leukocyte protease inhibitor; SLPI; asthma;
KW chronic bronchitis; pulmonary emphysema; respiratory obstruction.
XX
OS Synthetic.
XX
PN JP06228000-A.
XX
PD 16-AUG-1994.
XX
PF 28-JAN-1993; 93JP-0012652.
XX
PR 28-JAN-1993; 93JP-0012652.
XX
PA (TEIJ) TEIJIN LTD.
XX
DR WPI; 1994-299701/37.
XX
PT Agent to treat respiratory obstruction e.g. in asthma - contg.
PT polypeptide of specified sequence derived from secretory
PT leukocyte protease inhibitor
XX
PS Claim 2; Page 9; 12pp; Japanese.
XX
CC AAR58594 is the Arg59-Ala107 section of secretory leukocyte protease
CC inhibitor (SLPI), both it and the sequence described in AAR58595 can
CC used in the treatment of respiratory obstruction. Used orally or
CC parenterally they are particularly useful in the treatment of chronic
CC bronchitis, pulmonary emphysema and asthma.
XX
SQ Sequence 49 AA;

Query Match 41.6%; Score 136; DB 15; Length 49;
Best Local Similarity 51.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 12 KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVP 56
||| ||| : ||| ||| | | | | | | | | : | |
Db 2 KPGKCPVTYQQCLMLNPPNFCCEMDGQCKRDLKCCMGCMCGKSCVSP 46

RESULT 73
AAR75184
ID AAR75184 standard; peptide; 49 AA.
XX
AC AAR75184;
XX
DT 05-DEC-1995 (first entry)
XX
DE Secretory leukocyte protease inhibitor partial peptide.
XX
KW Secretory leukocyte protease inhibitor; interstitial pneumonia.
XX
OS Homo sapiens.
XX
PN JP07082168-A.
XX
PD 28-MAR-1995.
XX
PF 13-SEP-1993; 93JP-0227092.
XX
PR 13-SEP-1993; 93JP-0227092.
XX
PA (TEIJ) TEIJIN LTD.
XX
DR WPI; 1995-158906/21.

XX Effective treating agent for acute or chronic interstitial
PT pneumonia - contg. secretory leukocyte protease inhibitor
PT polypeptide.
XX Claim 1; Page 8; 11pp; Japanese.
XX A novel agent for treatment of interstitial pneumonia contains this
CC polypeptide or AAR75185 as an active agent. The peptides are partial
CC sequences of secretory leukocyte protease inhibitor (SLPI). In
CC particular, this polypeptide represents Arg59 to Ala107.
XX
SQ Sequence 49 AA;
Query Match 41.6%; Score 136; DB 16; Length 49;
Best Local Similarity 51.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
QY 12 KPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSCGMACFVP 56
Db 2 KPGKCPVTYGYQCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 46
RESULT 74
AAR66284
ID AAR66284 standard; protein; 49 AA.
XX
AC AAR66284;
DT 08-AUG-1995 (first entry)
XX Polypeptide fragment of Secretory leukocyte protease inhibitor.
DE SLPI; secretory leukocyte protease inhibitor; Arg58-Ala107;
KW fragment; treat respiratory tract obturation; neutrophil.
KW
XX Homo sapiens.
OS JP06298663-A.
PN 25-OCT-1994.
XX
PD 16-APR-1993; 93JP-0089933.
PF 16-APR-1993; 93JP-0089933.
PR (TEIJ) TEIJIN LTD.
XX
PA WPI; 1995-011756/02.
DR Treating respiratory tract obturation caused by neutrophil
XX endotoxins - using drug containing fragment of SLPT polypeptide
PT Claim 1; Page 11; 16pp; Japanese.
PS AAR66284 shows the amino acid sequence of SLPI (secretory leukocyte
XX protease inhibitor) from Arg at position 58 to Ala at position 107.
CC This polypeptide is used in a drug for treating respiratory tract
CC obturation, and is esp. useful for treating respiratory organ diseases
CC caused by neutrophils. A dose of 10 mg/kg of the polypeptide (as a
CC fusion protein) gave a change in the difference of the pressure of
CC the lung of 11.5 cm H2O after 9 min., compared ot 7.5 cm H2O for saline.
XX
SQ Sequence 49 AA;
Query Match 41.6%; Score 136; DB 16; Length 49;
Best Local Similarity 51.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
QY 12 KPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSCGMACFVP 56
Db 2 KPGKCPVTYGYQCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 46

RESULT 75
AAW01848
ID AAW01848 standard; peptide; 49 AA.
XX
AC AAW01848;
XX 28-OCT-1997 (first entry)
DT Antileukoprotease derived tryptase clara inhibitor.
XX Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral;
KW respiratory tract; lung disease; respiratory syncytial virus; RSV;
KW influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
KW exosporium glycoprotein.
XX Homo sapiens.
OS WO9703694-A1.
PN 06-FEB-1997.
XX
PF 24-JUL-1996; 96WO-JP02071.
XX
PR 24-JUL-1995; 95JP-0186094.
XX (TANB) TOKYO TANABE CO.
PA Beppu Y, Imamura Y, Kido H, Tashiro M;
XX WPI; 1997-132378/12.
DR Tryptase clara inhibitor comprises anti-leuko:protease fragment -
XX useful for treatment and prevention of tryptase clara activated
PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
PT and measles
XX Claim 2; Page 23; 40pp; Japanese.
PS AAW01843-W01851 are peptides derived from the C-terminal portion of
CC human antileukoprotease. The peptides inhibit the action of tryptase
CC clara. Tryptase clara is responsible for the activation of viruses that
CC have exosporium glycoproteins, such as those that infect the respiratory
CC tract. The peptides are useful for the treatment and prevention of, for
CC example, influenza, parainfluenza, respiratory syncytial virus (RSV),
CC mumps and measles.
XX Sequence 49 AA;
SQ Query Match 41.6%; Score 136; DB 18; Length 49;
Best Local Similarity 51.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
QY 12 KPGSCPIILIRCAMLNPPNRCCLKDTCPGIKKCCGSCGMACFVP 56
Db 2 KPGKCPVTYGYQCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 46
Search completed: February 11, 2003, 08:36:42
Job time : 39 secs

